

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
 TGCAGACTAAACCAGTCATTACTGTTCAAGAGCGTCTGCTAATCTACACTTTATTTCT
 TGGATCACTGGCGTTATCCTTCTTGAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCCTGCTACTGGTACCG
 TCATTATTCTTTGGGCACCTTGGTTGTTGCTACCTGCGAGCTCTGCATGGATGCTA
 AAACTGTATGCAATGTTCTGACTCTCGTTGGTCAACTGGTCGCTGCCATCGTAGG
 ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAGC
 AGTATAACTCTACAGGAGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAGGATT
 TCCTAAGAGTTGCTGAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
 ATGAAGGTTGTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
 ATTCCTTGGAGTTGCTTGCTTCCAAC TGATTGGAATCTTCTCGCCTACTGCCWCTCTG
 TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGCCTATTCTCT
 CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
 ACAACACTACTTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
 GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT
 TCATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTCTATCCCATTCAATGTTAGATCG
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FIGURE 2

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NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42



Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,



N-glycosylation site.

amino acids 134-138



Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCGTTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCGGAGGTAGAGAAAGTCAGT
GCCACAGCCCACCAGCGCTGCTCTGAGCCCTGGCACGCAGAACGGGAGGGAGTCTGAGGGT
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GCCGGGGTAGGCTCTGGAAAGGGCCGGAGAGAGGGTGGCGTTGGTCAGAACCTGAGAAACA
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GTTCCCTCTTCGGGGTCCTCACCAAGAGGTTCTGGGGTCGCCCTCTGAGGAGGCT
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TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTACCTAA**ATG**ATCGTCTTG
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GGCAGTAATAACGGACTCTGTAGATAAG**TAA**GTATCTGACTCACGGTCACCTCCAGTGGAAAT
GAAAAGTGTCTGCCCGAACCATGACTTAGGACTCCTCAGTTCTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTGATGTTTGCTGCTGTACACTTGTCTGGAAATGTCTAAATGTTTC
TGTAAGACGAGAAAACACGATAAGCTATGATCTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCI
AENSAVPTADTRSQRDPVRPPRRGRGPHEPRRKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCCTGTCCACCCGGGGCGTGGGAGTGAGGTACCA
GGCAGCGCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTC
TAACGGACTG
CAAGATGGGAGGAAGGCAGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTTCCCCGACACATACCTTCGGACTAGTGCAGAGCAAACCTCTCCCTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTTCACAGCATGCTTGGCTCAGCTCA
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GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACCAGGGTCCC
GATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC
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20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

FIGURE 6

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATT CAG ATT TAAG CCC ATT CTG CAG TGG AAT TC ATG AACT AGCA AGAGGAC ACC AT CTT
 CTT GT ATT AT ACA AGA AA AGG AGT GT ACCT ATC ACAC ACAG GGGG AAAA **ATG** CT CTT GG GT
 GCT AGG CCT CTA AT CCT CTG GG TT CTG GG ACT CGT AA AGG AAA ACT AA AG ATT GA AG
 AC AT CA CT GAT AAGT AC AT TT T AT CACT GG AT GT GACT CGGG CTT GG AA ACT TG GC AG CC
 AGA ACT TT GATA AAAA AGG GAT TC AT GT AAT CG CT GC CT GT CT GACT GA AT CAGG AT CA AC
 AG CT TT AA AGG CAG AA AC CT CAG AG AG ACT TC GT ACT GT GCT CT GG AT GT GAC CG ACC CAG
 AGA AT GT CA AG AGG ACT GCC AGT GG GT GA AGA ACCA AG TT GG GG AG AA AGG TCT CT GG GT
 CT GAT CA ATA AT GCT GG TGT CCC GG CGT GCT GG CT CC ACT GACT GG CT GAC ACT AG AGGA
 CT AC AG AGA AC CT ATT GA AGT GA AC CT GT TT GG ACT CAT CAGT GT GAC ACT AA AT AT GCT TC
 CT TT GG CT CA AG AA AG CT CA AG GG AG AG TT ATT AAT GT CT CC AGT GT GG AG GT CG C TT GCA
TE~~G~~ GT GG AG GG GG CT AT ACT CC AT CC AA AT AT GCA GT GG AAG GT TT CA AT GAC AG CT TA AG
 AC GG GAC AT GAA AG CT TT GG GT GC AC GT CT CAT GCA TT GAA CC AGG AT T GT CAA AAC AA
 ACT TGG CAG AT CC AGT AA AG GT AA TT GAAAAA ACT CG CC AT TT GG AG CAG CT GT CT CC A
 GAC AT CAA AAC A CA AT AT GG AGA AG GT TAC AT T GAAAAA AGT CT AG AC AA ACT GAA AGG CAA
 TAA AT CCT AT GT GA AC AT GG AC CT CT CCT CG GT GG TAG AGT GC AT GG ACC AC GCT CT AA CAA
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 TCT CAC AT GCC AG CAG CT TGT CA AG ACT TT TATT GT TGA AA AC AG AA AG CAG AG CT GG CT AA
 TCCC AAGG CAG TG **TGA** CT CAG CT AA CC AC AA AT GT CT CCT CC AGG CT AT GAA AT TGG CC GAT
 TTCA AGA AC AC AT CCT CTT CA ACCC ATT CCT AT CT GCT CC AA CCT GG ACT CATT AGA
 TCG TGT TATT GG ATT GCA AA AG GG AG TCC ACC AT CG CT GG GT AT CCC AGG GT CC CT G
 CT CA AG TT TCTT GAAA AGG AGGG CT GG AAT GGT AC AT CAC AT AGG CA AGT CCT GC C CT GT
 AT TT AGG CTT GC CT GCT GG GT GAT GT AAGG AA ATT GAA AG ACT TG CC C ATT CAA AA AT G
 AT CT TT ACC GT GG C CT GCCCC AT GCT TAT GG TCCC AG CATT AC AGT AA CT GT GA AT GT T
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FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
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AELANPKAV
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 **Important features of the protein:**

 **Signal peptide:**

amino acids 1-17


 **Transmembrane domain:**

amino acids 136-152


 **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256


Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**A**TGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGCGGGGCCCTTGGCCGTCGCCACCACT
 GTAGTCATGTACCCACCAGCCGCCGCTCATCGGACTTCATCTCGGTGACGCTGAG
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 GCTCATGGAGACTTGTACAGATGAACCGGCAGATGGAGACGGGCTGAGTCCCGAGATCG
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 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAACGCCACCCCTGCCTATCT
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 GGCGTCAGTCTGGTGTGATGCCAGGGCTGGCCGCTGGAGCCTCCGCTGCTTCTC
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FIGURE 10

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I A G L K P A N P P V L P A P Q K A D T D P E N L P E I S S Q K T Q R H I Q R G P P H L Q I R P P S Q D L K D G T Q E E A T
K R Q E A P V D P R P E G D P Q R T V I S W R G A V I E P E Q G T E L P S R R A E V P T K P P L P P A R T Q G T P V H L N Y
R Q K G V I D V F L H A W K G Y R K F A W G H D E L K P V S R S F S E W F G L G L T L I D A L D T M W I L G L R K E F E E A
R K W V S K K L H F E K D V D V N L F E S T I R I L G G L L S A Y H L S G D S L F L R K A E D F G N R L M P A F R T P S K I
P Y S D V N I G T G V A H P P R W T S D S T V A E V T S I Q L E F R E L S R I T G D K K F Q E A V E K V T Q H I H G L S G K
K D G L V P M F I N T H S G L F T H L G V F T L G A R A D S Y Y E Y L L K Q W I Q G G K Q E T Q L L E D Y V E A I E G V R T
H L L R H S E P S K L T F V G E L A H G R F S A K M D H L V C F L P G T L A L G V Y H G L P A S H M E L A Q E L M E T C Y Q
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W E T L Q S F S R F T R V P S G G Y S S I N N V Q D P Q K P E P R D K M E S F F L G E T I K Y L F L L F S D D P N L L S D
A Y V F N T E A H P L P I W T P A
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCGGAGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TCCCCCTCGCGGAGGAAAGCGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCGCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTCGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG
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FIGURE 12

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TTGYKTFRHLHDPAWRKRDQKRIAQQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

■

Signal peptide:

amino acids 1-42

■

Transmembrane domain:

amino acids 29-49 (type II)

■

N-glycosylation site.

amino acids 154-158

■

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATTTGCCTATCCACCTCCCCAAGCCCCTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGCCTTCTTCCCCCTCCTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGAGATAGGAAACAGAACAGGGTAGTGGGTGGCTAGGGGG
GCTGCCTATTAAAGTGGTTGTTATGATTCTTATACTAATTATAACAAAGATATTAAGGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCGCCGGGAAGGCCGTCTCCGGCCATAAGGCTCGGTGCCGCTGG
 GCCCGCCGCCGCGCTCTGCCGCCGGCTCCGGGCCGCTAGGCCAGTGCGCCGCG
 CTCGCCCGCAGGCCGCCGCAGC**ATG**GAGCCACCCGGACGCCGGGGCCGCGCA
 GCCGCCGCTGTTGCTGCCGTCTCGCTGTTAGCGCTGCTGCCGCTGGCTGGGAGGGCG
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 ATCAAAATTGGCAGAAAACACAAATATGTCATATCTTTTTAAAAAGTATTCA
 TTGAAGCAAGCAAATGAAAGCATTGACTGATTAAAATTGGTGTCTTAGATATT
 GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCCTAATGGAACCACATT
 TTTTCACTTAGCTTCTGTGGCATGTGTAATTGTTCTGCGGTTTAATCTCACAG
 TACTTATTCTGTCTGTCCTCAATAATATCACAAACAATATTCCAGTCATTAAATGGC
 TGCGATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNVLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTP
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVNNKGDFRPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILOSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GC GTGGGG**ATG**TCTAGGAGCTCGAAGGTGGT GCTGGGCCTCTCGGTGCTGCTGACGGC GGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATT CGTCTTTGGGAGAACAGATTA
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA
TCA**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAAACACGAGTTGTGTGTGTGTTGATCA
GGAGAGTAGCTTAGTATCTTCATCTTTTTGGTCACTGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGTCATATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTGGAAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTACTGAGAAGCAGTGGAGCTGTGAGAAGGAAGGG
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC
~~TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC~~

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVVKQQWDQQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTTACAGCCTGTTCAAGTGTGGCTTAATCGTCTCCACCAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATACAACCACGACGTATCTCGGG
 CCTGGGGTCCCCCATGATCGTGGGTCCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCCTGGCCTCTCGCTGGTAGCGTGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGGTCACCTGGTGCTTGCTTCTCCGTGACCGTATCA
 TCCTCATCGTGGAGCTGTGCCTGGCTCCAGGCCGCTCCCCCTGTCTGGCGCAACTCCCC
 ATCACCTTCGCCTGCTATGCGCCCTCTCTGCCTCTGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTCCCTGTCCCACGCCGTTCGCGGACCAAGGCCATGCCGCCACCTCTTCT
 CCTGCATCGCGTGTGGCTTACGCCACCGAACGGTGGACCCGGCCGGCCGGCGAG
~~AT~~CACTGGCTATATGCCACCGTACCGGGCTGCTGAAGGTGCTGGAGACCTCGTTGCCTG
 CATCATCTTCGCCTCATCAGCAGCCAAACCTGTACAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTCATCCTAGCGGCCATGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCTGTGGGGCTGGCCTGCTGTC
 TGTCCCTCTATGCCACGCCCTTGTCTCTGGCCCTTACCAAGTTCGATGAGAAGTATG
 GCCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCACTACGTGTGT
 GCCTGGGACGCCGACTGGCTGTGGCCATCCTGACGCCATCAACCTACTGGGTATGTGGC
~~T~~ACCTGGTGCACTCTGCCACCTGGTTTGTCAAGGTCTAAAGACTCTCCAAGAGGCTCC
 GTTCCCTCTCCAACCTCTTGTCTTGTGAGTTCTTATGGAGTACTTCTTCC
 TCCGCCTTCTGTCTTCTCTGTCTTCTGTCTCCCCTCCACCTTTCTTCTTCC
 CAATTCCCTGCACTCTAACAGTTCTGGATGCATCTTCTCCCTTCCCTTGCTGT
 TTCCTTCTGTGTGTTGTTGCCACATCCTGTTTCAACCCCTGAGCTGTTCTTTTT
 CTTTCTTCTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTGGGTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAAGTAGCTGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTCTT
 TTCCACTCTCTTTCTCATCTCTTCTGGTTGCCGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTCTCCTGTGTGCCCTGGAGCCCTGAGACTCTTCTCCTTGCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTGGGGGTGGGGTAGCTGGGATTGGGCCCTTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTTGGAGGTCAAGTAATTCCAATGGCGGGAGGCATTAAGCACCGACCCGGTCCCTAGG
 CCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAAATTGGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
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SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IAFAFISDPNLQHQPALEWCVAVYAICFILAIAIILNLGECTNVLPPIPFPSSLGALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```



Important features:



Transmembrane domains:



amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312



N-glycosylation site.



amino acids 66-69



Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCATGCCAGCTAATTTGTATTTAGTAGAGACGGGTTCAACCAGTGTGGCCAGGCTGGTC
 TTGAACCTCGTGCACCTCATGATCCGCTCACCTCGGCCCTCCAAAGTGCCTGGGATTACAGGCATGAGCCACTGACGC
 CTGGCCAGCCTATGCATTTAAGAAATTATTCGTATTAGGTGCTGCTAAACATTGGGCACTACAGTGACCA
 AACAGACTGAATTCCCAAGAGCCAAGACCAAGGAGACCAACAAGAAACAGGAAATGCAAAGAGACCA
 TTATTACTCACTATGACTAAGGGTCAAAAATGGGTACGTTGATGGAGAGTGATTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCCTGTACGAGGTGGTATTCAGCCAACTGGAAGAATGA
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTCACTACACTTTGGCCTGAGAA
 ATAGCATGGATTGGAGGAGGCTGGGGAACACCACTCTGCCGACCTGGGAGGAGGATTGAGGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGACAGGGTAGGAGCAGGGACTTGCAGGTGGAATCATTAGGTCTTATC
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGGTAATGCTGAGGTTGGAGGCCAGGCTAGATGGCACAG
 TGGTGGGTGATGCCAAAGGAAGAGTCAGGCCAGGGCAGACGGGGAGAAGGTGAGGGGTTGGTTCCA
 TCTGGCGAGCTGCGGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGAGAGGGAAAGGGAACTTAA
 AGAAGTCCTGGATGCCAACACTCTTCTCCCTCCTCTCCCTCCTCAGAGGTCTCACTCGTGGTTCTCAT
 TCCCTGCCCTGCCCTCATCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTTGTCTCGGGCCTG
 TCTGAATCTCATTGCTTCTGGAGGACATAATTACCTGCTCTAGCTTCTTACATCTACATTCCCTGTAG
 CCACTGGGACATATGTTGCTCTAGCTCTGCTCAGGGGACTGACTTTCTAATGGTGTACCAAGGTGAATGTTGGAGACACAGTC
 GCGATGCTGCCAAGTCCCAGGCAAGCCCTAACTATCCAGGAGATCGCTGCGCTGCCAGGTCCTCCCTGCATGGT
 ATGCAGCCCCCTCCAATGTTCTGGCACTTTGCTCTTCTCCCTCCGGTTGCACATCCCTTGAACCTGGAACTGTTCT
 GTGAGTACATGCTGGGTCTCCCTTCTCCCTGCTCAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTT
 ACATGGATCTAACTACTGCCACCCCTCCACCTCCCTGCACCTGTGCTCCCTGGCTGGTCTTACCAAGGCTTC
 TCCACCCCTCCCTATCTCAGGTATTCAGGCTGGTGAAGGACCACTGACCTGCTGCCCTGGAAATCAGCCT
 GCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCAGTGAECTCACCTGCTGCCCTGGAAATCAGCCT
 TTTCTCTCATTCAGACCTCAGCAGGGCAACAAGAGGCTCGTTGCAGCAGGAGTGGCTGAGCAGTTGCCA
 TCGCGGAAGCCAAGCTCGAGCATGGTCTCGGTGGATGGCAGGACTCCACTGATGACTCTATGAGGACT
 TTGCTGGGGAATGGACACAGACATGGCTGGCAGCTGCCCTGGAGCCTGAGAGGCACTGCTCACAGACCGTGTCCCCAGACA
 ACCGGTTCTCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGGCACTGCTCACAGACCGTGTCCCCAGACA
 CCCTGTGCTCTAGTCTGTGAGGATGGGTGTTGGCTCCCCGGCCGGCTGGCTCCAGCTGGCTGG
 GCGATGAGCTGCTCTGCCAAACTGCCCTGGAGGAAAGTGCCTTCCGAGCCTGGGCACTGGAGGCC
 AGGACTCACTCTACAACTGCCCTCACAGAGTCTGCCCTGGAGGAGGAGGAGGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTGCCAACACTAACGGGAGCTGGGAACGGCAGCGGCAAGCCTCTGACCTGCCCTTCTG
 GGGTGGTGCCTTAGATGAGGATGAGGAGGCCAGAGGAACAGTGAACCATCATGCCCTGGCAGTGGCATGCA
 TCCCCCGGCTGCTGCCAGGGCAGGCCACTGTGCCCCAGTGTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
 TAGAGGGCTCTGGAGCGCTCGCTTCTCGGTGTTGGCATGAAAGTGTGTTGGAGAGGAGGCCAGGGCTG
 GGCTGGGGGCGCATGTCCTGCCCTCACTGCCGGGCTTGGCCGGGGCTCTGGGCTGGCTACAG
 GCTGTGGCAGACAGTGTGTTCTAAATGCCACACACACATTTCTCTCGGATAATGTGAACCAACTA
 AGGGGGTTGTGACTGGCTGTGAGGGTGGGGAGGGCCAGCAACCCCCCACCCTCCCCATGCCCTC
 TCTCTCTGTTTCTTCTCACTTCCGAGTCCATGTCAGTGTGCTGTTGATAGAAATCACCCCCCAGCTGGAGGGCTGG
 CTCCCTGCCCTCCGGAGCCTATGGGTGAGCCGTCCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTTC
 ATTACCTCTCCATGTCCTAAATCTCTTTCTAAAGACAGAAGGTTTGGCTGTTTCAGTC
 GGATCTCTCTCTGGAGGTTGGAAATGATGAAAGCATGTACCCCTCACCTTTCTGGCCCTTAATGG
 GCCCTGGGCCCTTCCCAACCCCTCTAGGATGTGCCAGTGTGCTGGCCCTCACAGCCAGGCCGGCTGCC
 ATTACCGCAGAGCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTGCACAGAGCTGGACTTCATGTT
 CTTCTAGAGAGGCCACAAGAGGCCACAGGGTGGCCGGAGTTGTCAGCTGATGCCGCTGAGAGGCCAGGAAT
 TGTGCCAGTGTGAGTGCAGTCAGGAGTGTCTCTTCTGGGAGGAAAGAAGGTAGAGCCCTCTGCTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCGCCCCAGCCAGGGTGTAAATGCCACGCTAGTGGAGGCCCTGGCAG
 ATCCCTGCATCCAAGGTCACTGGACTGTACGTTTATGGTGTGGGAAGGGTGGCTTGAATTAAGGCC
 CTTGTAGGCTTGGCAGGTAAGAGGCCAACAGTAAGAACGAGAGGCCAACGGGACAAGCATTCTATATAAGT
 GGCTCATTAAGTGTATTTGTCTATTAAAGAATTGTTATTAAATAATAAAAATCTTGTAAATCTC
 TAAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCTCCTGCTCAGTGCAGACTGTACACTTAACCCATCTGTTCTAATGCACGA
 CAGATTCCCTTCAGACAGGACAACACTGTGATATTCACTGATTGAAACACCTCCTAAG
 CCTGAAGCTTCTGTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAAATGGCATAA
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCCCTTAAAAAAAACCAATACCAAAG
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTT
 TTAAAACAATGGAAAATAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTCAAGGCAGTCATTCCCCTCCTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTCTCAGTAACTCATCAGCAGAGCATTCTTGGCAGTCTAA
 AACCCACATCTACCATTCCACAAGCCTCCCTGATCCATAGCTTGTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCTCAGCACATCCCAATGCTACACC
 TGCTCTGCTTCAGAAAACCTCACTTGGCTTGGTCAATGACACCGTGAAAACCTCCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACACAAACAGTGAAGTAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAACAACTCTACAGCCTACCTTAAATTACCAATAATTCAAAACTCTTCCAA
 ATACGTCAAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTTAGGT
 GCTATTCTGGGTGTCATTGCTACTCTTGTGGCTACTGTTGTGGAAAAGGAAAAC
 GGATTCACTTCCCCTCGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
 ATGCACCGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAAGCCATGCCAGAAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTCTGTATTAGAACTAACAGAAAAAGCGTTAACAGCAAGTGTACATCTA
 CATCCTAGCCTTTGACAAATTCTACCTTCAAAAGTTACACAAAATTACTGTCACGTGGAT
 TTGTCAGGAGAATCATAAAAGCAGGAGACAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTCTACAAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
 TGTATTAGTAGTATTCTTAGTAGAAAATATTGTGGAATCAGATAAAACTAAAGATT
 TCACCATTACAGCCCTGCCTCATAACTAAATAAAAAATTATTCCACCAAAATTCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATATTCAAGATTGCAT
 TTTCTTAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTATAATTCTAGATCAGCACACATGATCAGCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCTACCCAGGAAAGTAATAGCT
 TCTTAAAAGTCTCAAAGTTGGAAATTAACTTGTCTTAATATCTTAGGCTTCAA
 TTATTTGGGTGCCTAAAAACTCAATGAGAATCATGGT

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGRKRTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSSYYNPTLNSA
MPESSEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCAGGCCAGGACGCTGATTCCAGCAGCGCCTACCGCGC
AGCCGAAGATTCACTATGGTAAAATGCCTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGGGCAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTA
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTCTGATAGTGACCCCTGCAG
CAATTATTGACTTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGAACACTGC
TATCTGATGCCCTCAATACTCTATTGTTATGCCTCCAAAAAACTGGTAGAGCTCTTGG
CAAACGGCGAGTGGCAGATATGCCTCAAACCTATGTGGTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTGATGTTAGTAACCTGGCATCTTATTACCAACTTGCACAAACAGA
AAGTCCTCCGCCTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTTACTCTATTGCTTATGCTT
AAAAAAAGGAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT
TGGCATTGCTTGTGAAACTGAAATTACATGAGTTCATTTTCTTGCATTATAG
GGTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAATTCCATCC
GTTGTTTTTGTGTTGTTGTTCTTCTTAAGTAAGCTTTATTCATCTTATG
GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATTATA
TCAGATCTAACATTGTTGGTTCTTGTGTTTCATTGTTGACAACTTCTGAAATTAGA
AATTACATCTTGCAGTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAAATT
TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCACTACTATCTGATTGTGG
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTGTATGAATTCTACAA
CCCTATAATAATTACTCTACAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSILRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIFYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACGGTCTGGGGCACCATGGTTCGGCGGCAGCCCCAGCCTCCTCATCCTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCTGGGG
 GCCCATCACCCCCCACCAACTCCTGGATGGATAGTGGACTTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAACAGAAGGCCCTGGCTATTACCATCGTCCTCCCCAAGAAGAAAGTAC
 GTGGACCAAGAGTGACCGGGCCGGGGCCCCGGGCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCGACATCTGGCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGGCCAGGAGGGGACCAGGAAGTCCA
 GGGACATGGGTCCCAGTGGAGACACCAGAGGCCAGGGAGCTGGAGGGTCTCTTGTAGCCCAG
 AGGGGCTGTGGTGGCGGTGAGGGCCAAGGGAGCTGGAGGGTCTCTTGTAGCCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCAG
 TGTTAACCAGTCCTCCGGCTGCCAGCCCTGACTGTCGGCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTGGCCTCCGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGATTACAGGCAGTGAGCCACCGTGCCGGCCAAACTACTTTAAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTCCTGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGACCTCCACCTGGGAAGTCCGAGGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGCCACCCCTGTTGCTCACACATTGTCAGCAGCCTG
 TGTCCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTTCTGCTTCTG
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAAGCACAATAACCTTATTCCGGCCTGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGLASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVPEAQUEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGCAGAGATG
 AAGTTCCAGGGGCCCTGGCCTGCCTGCTGGCCCTGCCTGGCAGTGGGAGGCTGG
 CCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCCAG
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
 GATGCTGTCCGGCTCCTGGCAGGGGTGCCTGGCACAGTGGTCTGGAAACTTCTGG
 AGGCCATGGCATTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTGAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGAATGGAGGCCACAAACTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGCCAGCAACCAGAACATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAACAATGGCAGCAGCAGTGG
 TGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCAGCAGTGGCAGCAGTGG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCAGCAGTGGCAGCAGTGG
 TCCAGCACCGCTCCTCCGGCAACCACGGTGGAGCGGGCGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGAATGAAGCCCGGGAGCAGGGAAATCTGGATTCAAGGGCTTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGGTACGCTGT
 TGGTGGAGTCATACTGTGAACTCTGAGACGTCTGGATGTTAACTTGACACTTCT
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACACAAGGACCAAGAGA
 AGCTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGAGGCCACACT
 CCCTCCTAAACACCACCCCTCTCATCACTAATCTCAGCCCTGCCCTGAAATAAACCTTA
 GCTGCCCAAAAAA
 AAAAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGGSSGGSSGGSSGGSSGSRGDGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNRYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGGTCCCTCCGGTCTGGATGTGCGGA^TCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG
 TGCCCTGGCTGGAGTTCTCTCCTTGCTGACC^ATGTTGTCAGGACTGAGGGAAAGAT**TG**TCTTCTGAACAAAGC
 CTCTCCTGCTGCCCTGCACCGGAGCTTGGTGTGCA^GAGACTGAGGGAAAGAT**TG**TCTTCTGAACAAAGC
 TGCTGCTACTTGCTGCTCTGGCTGGCTTCCAGATCCCACAGTCCCTGAGGACTTGTTCTTCTGAAGAG
 GTCCCTCATATGCCTTGAGGTGGACACAGTAGCCCAGAGCATGGCTTGACAA^TTGCGCCTGTGGTGGAC
 AGCTGCTCTACACCTGCTGCCCTACATCGAGAGCTCCGAA^ACTGCTGCTGGTGTCA^GAGCTAGTG
 GACGGAGTGGGGCTTCATGAGGAA^AATCACCC^CCCACACTACCAC^CAGCCTGGGAGGCCAGCCTCCCAGACCA
 GCCAGGGCTGCAGGCACAGCTGCCAGGCCCTTTCCACAACAGGCCCTCCTGCCGGACCGTAGAGT
 TCGTGGCAGAAAGAATTGGATCAA^ACTGTGTC^AACAT^ATAAGGCTACACTGGTGGCAGATCTGGTGC
 CAGAGTC^ACTTCTCCAAGAGCAGCTGGTGA^CACAGGGAGAGGAAGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCC^CAGCTGTGCC^CTCACGGGCCAGGCATTGGCC^TGGGGGGAGTTCTGTC^AAGGAAGGCCCTG
 GGGCTGTGCCGGCTGCTCCAGAGGAGACCCGGCAGGCC^TGTGAGCAGTCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTCA^GCCAA^ACATCACAGCA^TGTGATCAGGAGGGAGGTGA
 AGTCAGTCACACTTCGAGGCCAGGGCTGTGAACCTGCTGCCGGGGAGCGGAGGGGCTGCTCCGCC**TGAC**
 GTGCTCTCTGGCCGTGGGGCCACGGGACCC^TGACGAGGGAGTCTCCCAGAGCATCTGGAA^CAGCTCCTAGGC
 CAGCTGGGCCAGACGCTGCC^TGGGGCCAGTTCTGTGCC^CAC^TGTGAGCAGCATCTGGCAA^AGTGCTCTGTG
 GAGTTAGCTCCCTCCTCGTTGCA^GATCAA^ATTCTATCTAGGGCCCCGGCAGACTACAGGCTGGAGAGAGGG
 CAGGCTGAAGGCTCTGCACATGCTGCTTC^TTGTGGAAGGAAGACTTTCA^GGGGCCGGT^TCCGCTGAGCTG
 CTGCTGAGCC^AAGAA^AGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTGCTA
 CGGGAGCTGGTGGAGAAGGGCTGATGGGACGGATGGAGATAGAGG^CCTGCC^TGGGAGCCACCAGGGCCAG
 TGGCCAGGGACTTGTGAAGAATTAGCAACACTGTCTAATCTGTTCTAGGGCC^CCCACCTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAA^ACCGGGGCA^TGTGCTGCCAGAGCTAGGGCTGAGAAGTGGC
 CTGCC^TGGGCATTGCA^CAGAACCTGGACCCCCGCC^TACGAGGAGGCCAAGTGC^CCA^TGCAGACCCCTC
 TGGTGGGGTGTAGCTGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTACTGCC^TGGC^ATCCCACCAGCGA
 ATCC^TAGAGGAAGGAGAGTTGGCTGATTTGGGATTATGGCAGAA^AGTCCAGAGATGCCAGTC^TGGAGTAGAA
 GAGGTGGTGTGTTGTTATCTCTTGATACTAA^AATGAA^AGTGGGTGTG^TGGGCTTGTCAACACAGAA^ATCAAGCCT
 CATTGCTATCCCAGCATCTTAA^AACTTGTAGTCTTGAATT^ATGACAGAGGCCAATGACTCCTGCTTAAC
 TTATGAGAA^AATTTAA^ACTGAA^TCTTGGGAGTCTACATTCTTATCACCAGGAGTGGACTGCC^ATCTCC^T
 ATAATGCTAACACAGGCCGGCTGGTGGCTCATGCC^TGTAA^TCC^CACTTGA^GAGGGCTGAGGTGGCG
 GACTGCC^TGGAGTCAGGAATTCAAGAGCAGCTGCC^AACATGGC^AAA^ACCCCATCTACTAAA^AAAAAAA
 TTATAGCTGGCATGGGGTGTG^TGGCTGTAATCCCAGCTACTCAGGAGGATGAGG^CAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGCA^GTGAGGCCAGGT^CGACC^ACTGCA^TGGGTAACAGAGCGAGACTTCTAG
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCA^ACTGAA^ACTGACTTTCCCTGTA^CCTGCC^ACTG
 TGCAGGTAGTAACCTCTTGAGACCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTAGAATAAA
 CTGGTTTCTTAA^AAAAAAAGGGCGGCC^TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTAA^AAGGGCTTATTAA^AATCTCCCCACAGATGGCTCTGCA^ATCTGCCACAGCTC
 TGGGGCTGTCTGAGGAAAGGCC^TGT^TTTCCCTGAGGCCGGGCTGGGCTTGTCC^ATGGTCCGGAGCTG
 GCCGTGCTTGGGCC^TGGCGTGTCTAGCTGCTTCTGCCGGGACAGAGCTGCCGGTCTGGGGGCC^ACCGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGTGGAGGCC^TGTCTTAACCGACACC^TGTGAGGTGCTCTGAGATGCTG
 GGTCCACCC^TGTAGTGGCACGGGGAGCAGCTGTGCC^TGTCTCYTAGGCCAGTC^TGTGGGAAACTAAGCTC
 GGGCC^TCTTGTCAAAGAGCCAGGATGGGTGGGTGTGGGGACTCATGGGA^ATGCC^TGGAGCTACGTGT
 GAAGAGGGCGCCGGTTGGCTGAGGCC^TGTGGAGGCC^TCTC^TCTGAGCCTGAGCTCAGTTCCCTTCCGTCTA
 ATGAAGAACATGCC^TCTGGTGTCTCAGGCTATTAGGACTTGCC^TCTCAGGA^AGTGCC^TCTGGACGAGCGT^C
 CATGTTATTTCA^AACTGTCTGCC^TGGCACGTTGGCTGGGCCACGT^CATGGAA^AGTGCC^TCTGGACGAGCGT^C
 GTCGCC^TGGAGTCGCC^TGGCACGCCAGGGGGGCCAGACCTGCC^TGGGGTGA^GGGGGAGGCC^CCCGGAGGG
 CCTCACAGGAAGTTGGCTCCCGACCAC^AGGCAGGGGGCTCCGCCGCCGCC^CACCACCGTCCAGG
 GGCGGTAGACAAAGTGAAGTGC^TGGCTGGGCTGCTGCC^TAGCAGGTAGCC^TGTATGCC^TGTGAGCAGGCC
 TCGTCCGCCAGCTGGAAGCAGGCC^TCCACCAGCACGA^ACAGCC^TGTGCC^T

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGCTACTGAAGGCTGTCTGATCAGGAAACTG
 AAGACTCTCTGCTTTGCCACAGCAGTCAGCTGCAGCTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTAGCAGTGTCTGATCCTCTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCAAACAGTCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAAGACACTGCCCTCTGGTGCCACCAGTGTGTATTGTCAAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCTGAGATCGAGCAGGGCTGAGTGTACAATCCGATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACTACCGCGTGTGGCCATTCC
 AGTGTGTTCCCGTGTGAGGAGGCCAGGAGTTGTCAACCAGGACCCCTGAAACCGTGT
 CATCTCTGGGGGCCCGAGCAAGATGCAAGAGCCCCAGGGCAGCCTCGTGTGATCC
 AGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG
 CAATTGACGACCTCTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGTGACGCCAGGGCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCAAGGGCCGGACAATGTGTACCTACATCCAGAATGAGCACAGTCGAAGGG
 CAACCACCACCGCTTCATCACGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCGGACCT**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAACGCCTCCGCCAGCCCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTC
 TTGTGCAGTCAGGGCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTCCATGAGGCCCTGGTTAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGATAATGGGGTCTGTCTCCAAAGGAGCTGGAACTTGGTGTG
 CCCCTCAATTCCAGCACCAGAACAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAACATTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGAGGTCCCAGAGGTGG
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGGACAAACCCCTCCCCCTCTGG
 CACCCCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA
 GTGCCCTCGGGTCTGCTCTCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAAGGCT
 CAGCTCTTGGGGGTCTGGGGTGAACCTCCCCACCTCTGGAAAACCTTAGGGTATTTTG
 GCAAACCTCCTCAGGGTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTGGCTCTAAAGGGCCAGGCCCTCTTCTGCCCT
 CTAGCAGGGAGGTTTCCAACCTGTTGGAGGCGCCTTGGGGCTGCCCTTGTCTGGAGTCA
 CTGGGGCTCCGAGGGTCTCCCTGACCCCTGTCGTCTGGATGGCTGTGGAGCTGT
 ATCACCTGGGTCTGCTCCCTGGCTGTATCAGGCACATTAAAGCTGGGCTCAGTGG
 GGTGTGTTGTCTCTGCTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTATGGGTGG
 GGGCGGTGACTGCCCAAGACTGGTTGTAATGATTGTACAGGAATAAACACACACCTACGC
 TCCGGAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSHILLGTKLGPEIERAECTIRMNADPTTGYSAVGNKTTYRVVAH
SSVFRVLRRPQEfvNRTPETVFIFWGPPSKMQPKQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVVGMVPPNYCSQRPRILQRMPYH
YYEPKGDPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGAAGCATCCCTAGCTGTGGCGCAGAGGGCGAGGCTGAAGCCGAGTGGCCGAGGTGTCAGGGGCTGG
 GCCTAAAGGTGAAAGAGTTCAAGAACAGCTCTGGAACCCATGACCCATGAAGTCTTGTGACATTATACCGT
 CTGAGGGTAGCAGCTCAGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTGTCGACCTTACCGT
 GGCCTATGGGACGTTGGCTTCAGACCTTGTGATACACC**AT**GCTGCGTGGGACGGATGACGGCGTGGAGAGGAATG
 AGGCCTGAGGTACACTGGCTTGCCTCCTCAGGCCACAGCAGGCTGCTTGACTGTGATCTGGGCTGCGTGGTGGAACCTCCA
 AGGATGAATGTAACCTGGCGCTGAATGGAAGAGCTGAATGGCTGGATGATGCTCTGGGTGTCCTCATCACC
 CACGGGACCCCTCGTCATCACTGCCCTAACACACCACACTGTGGGACGGTACCGTGTGCCCCGGATGCCCTGCG
 GGGCTGTGGCCAGCGTGCAGCCTGTGACACTAGCCAATCTCAGGACTCAAGTAGTGTGACAGCTG
 ATTGAAGTGGATGAGGGAAACACAGCAGTCACTGGCTGCCACCTGCTGAGAGGCCACCCCAAAGCCCAGGTCCGG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCAGAGGTAACACTACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGGCCAGGAGGACGAGGGCATGTACAAGTGTGAGCCTACAACCCAGTGACCCAGGAAGTGA
 ACCCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCGATCATCTACCCCCCAGAGGCC
 CAAACCATCATCGTACCAAAGGCCAGACTCTCATTCTGAGTGTGCCCCAGTGGAAATCCCACCCACGGGTC
 ACCTGGGCAAGGATGGGTCAGTGTGACGGCTACAAACAAGACGCCCTCTCTGCTGAGCAACCTCCATCGAC
 ACCACAGCGAGGAGGACTCAGGCCACCTACCGTGCATGGCCGACAATGGGTTGGGAGGCCGGGAGCGGTC
 ATCCTCTACAATGTCCAGGTGTTGAACCCCCCTGAGGTACCATGGAGCTATCCAGCTGGTCATCCCCGG
 CAGAGTGCACAGCTTACCTGTGAGGTGCGTGGGAAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCATCTCCAGGCCAGCGCCTCCGGCTCTCCGCAGGGCCCTGCGCGTGCAGCATGGGCGCTGAGGACGAAGGC
 GTCTACCACTGTCATGGCGAGAACAGAGGTGAGGCGCCATGCCGTAGTCCAGCTGCCAACCTCCAGGCAAGC
 ATAACCCCCAAGGATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC
 CCTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCGCAGGCTCCCATACCTCTCAGCTCGCCCCGCAACCTCCAAGACAGAC
 CCAGGAGAGAAGGGGCAAGGGGCTCCCGCAGGCTCCCATACCTCTCAGCTCGCCCCGCAACCTCCAAGACAGAC
 TCATATGAACTGGTGTGGCGGCCTCGGCATGAGGGCAGTGGCCGGCGCAATCTCTACTATGTGGTGA
 CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACCAAGCACGCCCTGACCC
 ACCAGACTTGACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACACTGTGCGGGAGAGGGCAGACAGCC
 ATGGTCACCTTCCGAACTGGACGGCGCCAAACCCGAGATCATGGGCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCCGGAGGGCAGCAGCTCCCGAGACAGCAGCCAGCACGGCCGCTCTCCCCCCCAGAAGCTCCCGACAGG
 CCCACCATCTCACGCCCTCCGAGACCATCTGAGCTGACCTGGATTCTGGCCACAGGCCATCCCCCA
 CAGTCCTTCCGTGGAGTACAAGAAGCTAAAGAAAGTGGAGACTGGATTCTGGCCACAGGCCATCCCCCA
 TCGCGCTGTCCGTGGAGATCACGGCCCTAGAGAAAGGCACCTCTACAAGTTGAGTCCGGCTCTGAACATG
 CTGGGGGAGAGCGAGCCCAGCGCCCCCTCTCGCCCTACGTGGTGTGGCTACAGCGGTGCGTGTACGAGAGG
 CCCGTGGCAGGTCCCTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAACAACAAACACCCAACTCCATGGCTTATATCTATTATCGACCCACAGACAGTGA
 GACAATGATAGT
 GACTACAAGAAGGATATGGGAGGGGACAAGTACTGGCACTTCCATCAGGCCACCTGCGAGGAGACCTCCTAC
 GACATTAAGATGCACTGGCTCAATGAAGGAGGGGAGAGCGAGTTCAGCACACGAGATCTGAGACCAAAGCT
 CGGAAGTCTTGGCCAGGCTGGTCACTGCCACCCCCAACATCTGGGCCCCACACAGGCCGCCCCCTCTGAA
 ATAGAGCGGCCGGTGGCACTGGGGCATGGTGGCTCGCTCAGCGACCTGCCCTATCTGATTGTGGGGTGT
 CTGGGCTCCATCGTCTCATCATGTCACCTCATCCCCCTCTGTTGTGGAGGGCTGGTCAAGAAAAACAT
 ACAACAGACCTGGTTTCTCGAAGTGCCCTCCACCCCTCTGCCGTTACTATGGTGCATTGGGAGGACTC
 CCAGGCCACAGGCCAGCTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCTCGGCTGAGTGGCTACCCGGCATGAAGCCCCAGCAGCAGTCCAGGCGAGCTTCA
 CAGCAGAGTGCACCCAGCAGCTGAGGAGACCCATCTGGCAATGGATATGACCCCCAAAGTCACCAAGATC
 ACGAGGGTCCAAGTCTAGCCGGACAGGGCTTTCTTATAACACACTGCCCGACGACTCCACTCACCAGCTG
 CTGAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGTGAGGAGAGCC
 CCCGACAGTCTGTCTGGAAAGCAGTGTGGGACCCCTCATTCTACTCAGGGCCCCCATGCTGCTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCCTGACTCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCGTAGGG
 GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCACTGGTGGCTGTGTTGAAACACCC
 CTCACAATT**TAG**GCAGAAAGCTGATATCCCAGAAAGACTATATATTGTTTTTTTTAAGAAAAAGAAGAAAA
 AGAGACAGAGAAATGGTATTATTTCTATTATAGCCATATTATATTTATGACTTGTAAATAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCCTACCGCTGGAGGTTGGAGAGGGAAAATAAGAAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGGGACAGACTCTAACCTGGGCTCTGCAGTG
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGTTCATCAGGAGCA
 TGAGGGAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCGGTGCTACGGGAA
 ACATTTCCTAAGATGCCCATGAGAACAGACCAAGATGTGACAGCACTATGAGCATTAAAAACCTTCCAGAAT
 CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAGTCTTCCCTGTAAAA

FIGURE 36

MLRGTMATWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLVRSTAEEAARIIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERGNPPPSVLWLRNAVPLISSQLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVVQLRTSRPSITPRLWQDAELATGTPVSPSK
 LGNPEQMLRGQPALPRPPTSVGAPSPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGI PANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNT
 PIHGFYIYYRPTDSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDL PYLIVGVVLGSIVL
 IIVTFIPFCLWRAWSKQKHTTDLGFP RSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGE LQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHDCCQRQE QPAAVGQSGVRRAPDSPV LEAVWDPPFHSG
 PPCCIGLVPVEEV DSDSCQVSGGDWC PQHPVGAYVGQEPGMQLSPGPLVRVS FETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGCCCTGCCCATGCCCTGCTCCTC
 CCAGGCTCCCGGGCGACCCCCGCGAACATGCAGCCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCCAGC
 CCGTAACCCGCGGGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC
 AGCCTCTTACCAACGCCGGGTGTCCCCAGCGCCCTCACTACCCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG
 TGGACGGCCACAATGACCTGCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGCCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTCCTACTCTGAACCTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCTGCCCTATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCGCT
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGTCCTATGCATCGGACACCTTGATAAGAAGGGCTGG
 AAGTGTCTCAGGCTCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATGTGATGGTGACACT
 GTCCATGGGGTGCTGCAGTGCAACCTGCTAACGTGTCCTGTGGCAGATCACTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGAAATTATGACGGGACT
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGCTCGTGGAAACCTGCTGGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGTCTCAAATGCC
 CCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAAACCTCACCCAGTGGCTC
 TGTGACACAGTCGGCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRRLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLA CLIGVXGGHSLDSSLVLSFYVLGVRYLTLCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDL SYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKvreESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGCCGGCTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTCCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTACATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCAGTGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGCTTCTTGGGCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCCTGGCTCCACTCTG
 CGCCTTCCAGCTCTGAGTCTGGGAATGTTGTTACCTGGAAAGATAAAAGCTGGTCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCCCTGAGTG
 GTTCTTATCACCAACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGG
 AGCTGGTGTGCTGCCCCGTGCACTTCTGCACTGGGCATGGAGTGCCATGCATACT
 CTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGCTGGCAGTCCCTCCTCCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTCGGTTGAAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCTGTACTTGGGTTGCCCTTGTCCCTGAACCTCGTTGTAACAGTGCATGGA
 GAGAAAATTGTCCTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
 TTTTATTTCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDVAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTGGGTCGCTAATTCGTCCGTAGGGCGTGAGACTGAGTTCATAGGGTCTGGTCCCCGA
 ACCAGGAAGGGTGAGGAACACAATCTGCAAGCCCCCGCACCAAGTGAGGGGCCCGTGTGGGTCTCCC
 TCCCTTGCAATTCCCACCCCTCCGGGTTGCGTCTTCTGGGACCCCTGCCGGAG**ATG**GCCCGTTGATG
 CGGAGCAAGGATTGCTCTGCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGAGT
 TCGCGGGCCAACCTCAACTCCATCAAGTCCTCTGGCGGGAGACGCCTGGTCAAGGCCAACATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTGGCGCAGTAAGAAGGGCAAAACCTGGGGCAGGCCAACCTGGTAGCAGT
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCAACAGGATCATGGCCTGCAATGGTGTGCGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGATCCCAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTGCTGGATGGTACTGGCACAGAGATCGAAACCACGGTATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTGTCATTTCTGGACAAAATCTGCAAA
 CCAGTGTCCATCAGGGGAAGTCTGTACCAAACAAGCAAGAAGGGTCTCATGGGCTGAAATTTCAGCGT
 TGCGACTGTGCGAAGGGCCTGTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTCAAGAAAATT**TGAT**CACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAGAAAATGAACGTAAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CAACTGTCTATGTAATAATGTACACATTGTGAAAATGCTATTATAAGAGAACAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTCTCAGATTGCTGATTG
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTAGAGTTAACAAAATACTCCCTAGAATAACTTGT
 TACAATAGGTTCTAAAATAAAATTGCTAAACAAGAAATGAAAACATGGAGCATGTTAATTACAACAGAAAAT
 TACCTTTGATTGTAACACTACTCTGCTGTCATCAAGAGTCTGGTAGATAAGAAAAAAATCAGTCATAT
 TTCCAATAATTGCAAAATAATGGCCAGTTAGGAAAGGCCCTTAGGAAGGACAATAAAACAAACAAACAG
 CCACAAATACTTTTTCAAATTGTTACCTGTAATTAAATAAGAACTGATAACAGACAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATCTCTTTATCCTATGTGATTCTGCTGCAATGCTATTATTTCCA
 AACTATACCCATAAAATTGTAAGACTAAATACTTACACAGAGCAGAATTTCACAGATGGCAAAAATTTAAA
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTCTAAAGATTGGCATAACCTATATT
 GATAGAATTAGATTGTTAAATCATGTATTCATACATACTCTGTTGAGGTTGGCAACACATAGATCATATGT
 CACTGGAGTAAGCAAGAAAATTGGGAAACTTTGTTGAGGTTGGCAACACATAGATCATATGT
 AGGCACAAGTTGGCTGTCATTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGATGGGATTGCTAT
 CATAATATTACTATGCAGATGAATTCAAGTGTGAGGTCTGTGCTGACTATCCTCAAATTATTATTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCAAAAATGACTCCTGAACTAGACAGAGTAGTGAGG
 TTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTCCAAACCTCTGCAGCATCTG
 CTTATTGCCAAAGGGCTAGTTGGTTCTGCAGCCATTGGTTAAAAAATATAAGTAGGATAACTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAACCAACTTACTACTTTTAAACTT
 AACTCAGTCTAAATACTTGTCTGGAGCACAAAACAATAAAAGGTATCTTATAGTCGTGACTTAAACTTTG
 TAGACCACAATTCACTTTAGTTCTTTACTTAAATCCATGCACTCTAAATTAAAGTTCTCCAGTAG
 AGATTGAGTTGAGCCTGTATATCTAAACTTCCACATATTTACTAAGATGATTAAGACTTA
 CATTTCCTGCACAGGTCTGCAAAACAAAATATAAAACTAGTCCATCCAAGAACCAAGTTGTATAAACAGGT
 TGCTATAAGCTGTGAAATGAAAATGGAACATTCATCAACATTCTCTATATAACAATTATTATTTACAAT
 TTGGTTCTGCAATATTCTTATGTCCACCCCTTTAAAATTATTATTTGAAGTAATTTCAGGAAATG
 TTAATGAGATGTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATTTGCAGCTATTGAC
 TTTGTAATTAGGAAAATGTATAAAAGATAAAATCTATTAAATTCTCCTCTAAACACTGAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTEISLTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGT GATCCGCC TGACCTTGTAATCCACCTACCTGGCCTCCAAA
 GTGTTGGATTACAGGC GTGAGCCACC CGGCCGGCCAACATCACGTTTTAAAAATTGATT
 TCTTCAAATT CATGGCAAATATTC C CTTAAC TTCTTATGT CAGAATGAGGAAGGA
 TAGCTGCATTATTAGTCAGTTTCATTGCATAGTAATATTTCATGTAGTATTCTAAG
 TTATATTTAGTAATT CATATGTTAGATTATAGGTTAACATACTTGTGAAAATACTTG
ATGTGTTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT
 TTTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGGCCAGTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCC TACA ACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCCT
 CCTGGTTGGAGTCCTTCCCTCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAAGCTTTGCAGCTTCCAGCAGCACCATTGAAAATATCTGTGCTG
 TCCACCAGCCACAGCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGT CAGAACCTCTCTCTGAATTGGATCAGCTCAAGCAGTG
 AAAATAGTAATCAGATTCCATCAGCTGTATTGAAAGTCTTAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGT CATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGT CAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGT CATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTACGTGA
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTG TAAAAGCAGCCCTTTGCTTTTGT
 TTTGGACCAGGTGTTGGCTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAGTCAGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGEAPPKMANITSSQILDQLKAPSLGQFTTP
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHIDFKSQPEPSPVILSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSLNSASPAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLL SWLVPTKQRKRIA HVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

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FIGURE 45

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGGCC**ATG**GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGCTCTGCAGAGCTCTGCTGTTCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCGCGCTTCTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGGG
 GTCCCGCACCGACCGCGCGACCGCCTGCTGGACCTCTACCGTCGGCGAGCGCCGCGCTA
 CGGGCCCCTTTCTGCGCACCGCGTGGCTGGCGCGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCAATTACTGTGGCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCACGC
 GGAGCCGCCCCCCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCCCAG
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCCAGCAGCTGGCTACGTGCTGGCACGCTGCTGCTTCCATCCTGCTACTGGTCAC
 TGTCCTCCTGGCCGCCGCAGGCGCCGGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT
GCAAATAGGGAGGCCCTGGCTCCTGGCTGGCTGGCCAGCAGCTGCACCTCTGTCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGCTTGGTGGC
 AGCATAGCCCCCACCCCTGCGGCTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAACC
 AAAATCCCACGTGCCCACATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG
 AAGACATTCTGGAGGACACTCCCACATCAGAACCTGGCAGCCCCAAAATGGGTGAGCCTCA
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCACATCAGAACCTGGCAGCCTGAAGTTGGGCTAGCCTCGGAGGAGTCCCAC
 CCTCCTGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTGTGTTG
 CTTGGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCTACCCCTACCCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCCCT
 GGACTCTGCCCTGGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTCTGACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTGGGCTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAAAAA
 AAAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
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PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIEPLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAE PHEA PPPRGSPGNGSSHSGAPGPDP TLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDL DKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGGGCGTGGCGCAGCGGCGAC **ATGCCGTTGTCAGAGGACGACTTT**
 CAGCACAGTCAAACCTCACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCAGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGCATTGGCAGTCTACTGCCATGGAACCTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCCACCAGGG
 GGACCCCTGAGGGCTCAGACATCCTGAACACTACTTGAGAGCTACCTTGCCGTTGCCTCCACCG
 TGCCCTCCATGCTGCTGGCAACTTCCCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCCTGGCATTCTCATGGTGATAACTGCACTGGTGAA
 GGTGGACACTTCCTCCTGGACCCGTGGTTTTTGCGGTACCATGGTCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCCTATG
 AGGAACCTCCAAGCAGTGTATCAGGAGGAGCCATGGGGGGACGGTCAGGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTCCTGACGG
 CCACCATCTCCTCGTGCATGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCCTGTTCTGCGGCCATGTGTTCTGGTGAAGAGGAGCTCCCCA
 GGACTCCCTCAGTGCCCTCGGTGGCCTCCAGATTGATTCCCACACACCCCCCTCTCC
 GCCCCATCCTGAAGAACAGGCCAGCCTGGCCTCTGTGTACCTACGTCTTCTCATCACC
 AGCCTCATCTACCCGCCGTCGACCAACATCGAGTCCTCAACAAGGGCTGGGCTCACT
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTCCTCTGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCAGGTGCCAGGGCCAACAGCAAGGCCGTCCCAGGG
 TTCGTGCTCCTCGGACCTGCCTCATCCCCCTTCTCGTGTCTGTAACCTACAGCCCCGCGT
 CCACCTGAAGACTGTGGTCTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCTCTACGGGCTTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTATGTCCTTTATGTGTGCTGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCCTGGTGACCTCATC **TAGAAGGGAGGACACAAGGACATTGGTG**
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAAGGAGGGCTGGGGCCATGGAGGAAGGCC
 TAAAGTTCACTTGGGACAGAGAGCAGACACTCAGGGCTCATCCCTCCAAAGATGCCA
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAAGAACACT
 CCTGAGACAGTTGAAGAAGAAATGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCCACCTCTTCTAGCCCTCAAAGATGCTGCCAGTGGCTGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGCTTTGCAACCTCCAGCTGCGCTCATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCCCTGAAGGGTCTCCCTGGAAATGGA
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAACAACTGCCACTAACAGAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGCCCTGGG
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC
 TTTCAGTGGTCCCTGTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAAACTTGC
 GTATTCAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFPSLGI
GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAESTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLG
CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGCCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTC**ATG**CCCCATTGCCCTGCACCTCCTCGCCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGCTGGATTGGGAGCTGGAGGCCATGCGATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGCCACTGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCAGCTGGCTGCAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTCTGGAATATCTTCTCGGGAGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTATCTAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCAGCGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCCTGCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTCCGCAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCCACTCAAACACCGATGCCCGCGCATGATTTCTACCCGCCGC
 CGCGCAGGGCGCGCTGCTGGCCTCGTACACGTGGCGACGCCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCCTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGCGTGCGCCAGCTCTGGACGGCACCGCGCTCGTCAAGCGTTGGCGAGGACCGACA
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTGCCTGGCGAGCACACCGCTACCCGCACGGCTGGTGG
 GACGGCGGTCAAGTCGGCGCTCGCGCCGCATCAAGATCAACAGCCGAAGGGCCTGCAT
 CGGACACGCCAGCCCCGAGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTCGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVVLLTASGPRAVKRITFSPPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIVFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGCCGGCCTTCTGCCTGC**A**
GGACGCTCTGAAGCCACCCCTGTCTGGAGGAACCACGAGCAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGAGCCGGAAAGCCCCCATTCACTAGAACGACTGAGAGATGCGGCCCTCGCAGGGCTGAATTCCCT
 GCTGCTGTCACAAAGATGCTTTATCTTAACCTTTGTTTCCCCACTTCCGACCCGGCGTTGATCTGCAT
 CCTGACATTGGAGCTGCCATCTTGTGGCTGATCACAGACCTCAACCCGCTTACCTCTTGACCTGAA
 CAATCAGTCTGTGGAAATTGAGGGAGGAGCACGGAAGGGGTTTCCCAGAAGAACAAATGACCTAACAGTTGCTG
 CTTCTCAGATGCCAACGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTGGG
 ATATAGAAAACCAAACAGCCTACAGATGGCTATCTTACAAACAGGTGTCGATAGAGCAGAGTACCTGGGTC
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 GATCATCTCGAATTGGCTGTTACACGTAACAGCTATGGTAGCTGTACCTCTGTATGACACACCCAAAAGG
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTGTACACACCCAAAAGGATTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTCACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACCT
 AAAACCTGTGCCTCTAGCCAGAACAGACCTGAGCGTCATCTGCTTACCCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAATGCTGTCGCTTCTCAAATGTGAGGATGCTTATGAGCC
 CACTCCTGATGATGTGCCATATCCTACCCCTCTGGTCATATGTTGAGAGGATTGACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTCCAAGGGGATATCGGTTGCTGGCTGACGACATGAAGACTTGAAGCC
 CACATTGTTCCCGCGGTGCGCTGACTCCTAACAGGATCTACGATAAGGTACAAATGAGGCCAACACCCCT
 GAAGAAGTTCTTGTGAGGCTGTTCAAAAGGTTACATCAGGATGATA
 TTTCTGGGACAAGCTCATTTGCAAAGATCAGGACAGCCTGGCGAAGGGTCGTGTAATTGTCAGTGGAGC
 TGCCCCCATGTCCACTTCAGTCAGATTCTCCGGGAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
 AACAGAATGCACAGGTGGCTGACATTACATTACCTGGGACTGGACATCAGGTACAGTGGGTGCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACTACTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTTGTCAAAGGATACCTGAAGGACCCCTGAGAAGAACACAGGAAGGCCCTGGACAGTGATGGCTG
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCGAATGAAACTCTGAAGATCATCGACCCTGGTAAAGAACATT
 CAAGCTGGCCAAGGAGAACATACATTGACACCAGAGATAGAAAATATCTACAAACAGGAGTCACCCAGTGT
 AATTGTTGTACACGGGGAGAGCTACGGTCATCCTTAGTGGAGTGGTCTCTGACACAGATGTACTTCCCTC
 ATTGCAAGGCTTGGGCTCTTGAGGAACTGTGCAAAACCAAGTTGAAAGGAAAGCCATT
 AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCTTAAACTTTGAAACAGGTCAAAGCATTGTTCTCATCC
 AGAGCCATTTCATGAAAATGGCTCTGACACCAACATTGAAAGCAAAGCGAGGAGCTTCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAGG**ATAAGGTACTTAAGTACCTGCCGCCACTG
 TGCACTGCTTGTGAGAAAATGGATAAAAACATTCTTACATTGTTGCTTCTCTCTTACCTTAAACC
 TGTTAAACTCTAAAGCCATAGCTTTGTTTATATTGAGACATATAATGTGAAACTTAGTCCCAAATAATCA
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 GATCCCAGTTATGTTCTGTGTCCTCCTCATGATTCCAACCTTAATAACTATTAGTAACCACAAGTCAAGGGT
 CAAAGGGACCCCTGTGCCTCTTGTGTTGTGATAAACATAACTGCCAACAGTCTATGCTATT
 TCTCTACTGTCAAACTAAGAGATTAAATTCTGAAAAACTGCTTACAATTGTTCTAGCCACTCCAC
 AAACCACTAAAATTAGTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCCTCGATGCTCTT
 CTGCGTAAATTAAATTGTTGACTGAAGGGAAAAGGTTGATCATACCAACATTCCCTAAACTCTAGTTAGATA
 TCTGACTTGGGAGTATTAATTGGGTCTATGACATACTGTCCAAAGGAATGCTGTTCTAAAGCATT
 CAGTAGGAACCTGGGGAGTAAATCTGTCCTACAGTTGCTGAGCTGGAAGCTGTGGGGAGGGAGTTGACA
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAAACCTCCTGAACGGAAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTCTACTTGTAATGTAAGTCTTAAAATAAC
 TATTACAGATAAAAAAA

FIGURE 52

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<subunit 1 of 1, 739 aa, 1 stop
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CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPWEWIISELACYTYSMVAAPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIILMDPFDDDLKQRGEKSGIEIILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELQKGIIRHDSFWDKLIFAKIQDSLGGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKETQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIEINIYNR
SQPVLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGC GGAGGCC GCGGCGAGCCGGCGAGCAGTGAGGGCCCTAGCGGGGCCAGCGGG
 CCCGGGCCCTAAGCCATT CCTGAAGTCATGGGCTGCCAGGACATTGGTACCCGCCAAT
 CCGGT**ATGG**ACGACTGGAAGCCCAGCCCCCATCAAGCCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCCAGGAGATTCTGTCA
 GACAGGGGCCGTGCTTTCTGCTGGTACTGTCATTGTCATATCAAGTTGATCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCCACGGCGCAGAGCAGTGGTCCCCGGCGGGCTGGACGTAGA
 GGTGTATTCAAGTCGCAAGTATATGTGGCAGTGGATGGCACACCACGGTGTGGAGGATG
 AGGCCGGGAGCAGGCCGGGCATCCATGTCAATTGTCCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTCTATTCC
 CAACATGGTAGGCCCGGCCAGTGCATCTGCACTGTCAAGGATGAGGGCTCCTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGGCCAGGCTGCCCTGGGC
 TGGAGGGACACATGGCCTTGTGGAGCAGAAAAGGAGGGCCTGTCTCGGGAGAACATT
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGGCAGAGTGCCTGGCAGACACAGAGCTGAACCGTCGCCGGCGC
 TTCTGCAGCAAAGTGTAGGGCTATGGAAGTGTATGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAG
 GGAACCGACCCATTACCTGTACAGGATGCTGCGCTCTGCTTCAGCCCAGGGGTGTCT
 CCTCAGATGATAACAGTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGGGACT
 GTTGGTCTGAGGGCATCCAGCATACTCCATCAGCATCAAGAATGCCCGGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTCAGTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCCTGGCTGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCAAGTGGCCTACACCGGAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCATCAACACGCCGGCGAGAGTGCATCATCCCTGACG
 TTCCCGATCCTACCACTTGGCATCGCCTCAACATGAATGGCTACTTCAAGGAGGCC
 TACTTCAGAAGCACAAGTTCAACACGGTTCCAGGTGTCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCTGTGAAGACTCTTCTGCCAGACACAGAGGCCACACCTACGTGGCC
 TTTATTGAAATGGAGAAAGATGATGACTTCACCATGGACCCAGCTGCCAAGTGCCTCCA
 TATCTGGACCTGGATGTGCGTGGCAACCATCGGGCCTGTGGAGATTGTTCGGAAGAAGA
 ACCACTCCTGGTGGTGGGGTCCCAGGCTTCCACTCAGTGAAGAACGCCACCCCTCAGTC
 ACCCCAAATTCTGGAGGCCACCCCCAAAGGAGGAGGGAGCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCCTCCAGGACCCCTGCCAGGGCTGGTACTGTGTACCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGCTACCTGTTTAACA
 TGAGACTTAATTACTCAAGGGAGGGTCCCTGCTCCACACCCGTTCTGAGTT
 AAAAGTCTATTATTACTTCTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTCACTTCCAGGCCTGGCTCAGAATCTA
 ACCTATTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGTCACAGACTCACTCAGAGACCCTTA
 GACACTGGACCAGGCCCTCTCAGCCTCTTGTCCAGATTCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAAGCCCTCTGGAAAAA

FIGURE 54

```
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><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGPFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRLRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKHKFNTVPGVQLRNVDLSKKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVRGNHRGLWRLFRKKNH
FLVVGVPAASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGCTGGTGGAAAGGCCTAAAGAACTGGAAAGCCACTCTCTGGAACCACAC
 CTGTTAAAGAACCTAACGACCATTAAAGCCACTGGAAATTGTTGTCTAGTGTTGTGGGTGAATA
 AAGGAGGGCAGA**ATG**GATTCATCTCATTAGCCTGCTCTGGCTATGTTGGTGGATGTTA
 CGTGGCCGGAATCATCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTTGG
 GTGCTGGCCTCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
 GATATTCTTGAGGGAAAACACCAACAGCAAGTAAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCATATTGGTG
 TTTCCCTGTTCTGGGCTTCGTTCATGTTGCTGGTGGACAGATTGGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAATCACCACACGCTGGGTCTGGGTGTCCA
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACAGCAGTGTCCAGTTAATTG
 TGTTGTGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTCTTGTGATGCATGCT
 GGCTTAGAGCGGAATCGAACATCAGAAAGCAGCTGCTGGTCTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTCTCTGCCGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCACAGCCACAAGCCCAGGCCACGGGAGGGAGAGCCTCAGCCGCTGGAAGTGGCAGCCCT
 GGTTCTGGGTTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC
 CTTGGTCCAGGGCCTTGCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCAGTC
 TCTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCCAGAGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGAGCTATAGACATCCATTGTGT
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 GAATTAGTTAAGAAAAGAGGAGAACTTCATACACTACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTT
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 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTAGCATCTGTCAAGTTCTCCTTGCAGAAT
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 TCTTCAGGGCAGTGGACGTAGTTGAGCTTGTGAGGTTCTATGACGCATAAGCTAGCATGCCTATG
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 GGCCACAGTGGAGGAAAGTAGCACAATAGGATACAGTTGATGTAGTCATTGGCAACAATTGCATACA
 ATTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTCCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTTCAAAACTATATGGTTGCCTAGATTCTCTGGA
 AACTGACTTGTCAAATAAGCAGATTGAGCTAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATHVLPVGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAG**ATG**ATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGAGCAGCTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGGGTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTCAAAGAACAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTCCAGAGACCTGA
 GTGAAAACAAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAAGGGAAACGTGCTGGTAACAGCAA
 GTCCCAGACACCAGCCCCCAGTTCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCAGGAG
 CCAGGCCGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGGCTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
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 GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
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 AATCATACTC**TGA**ATTGAACTGGAATCACATATTCCACAACAGGGCCGAAGAGAGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNQRQQQLQALSEPQPRLQAAGLPHTEPQGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPEGRQVVEDRPVGGRGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRTDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GG**ATG**CAGAAAGCCTCAGTGGCTCTCCCTGGCTGGGCTGCTTCCTCTTACGCTGGCATTGCCCTTTCA
 CCAGTGGCTTCCTGCTCACCGTTGGAGCTACCAACCATA**G**CAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC
 TGCCATGGGGAGCCAAGGGAAACTGGGCCCTGCTGGATGGCTCCGATTTCGGGGTTGTGTTGGTGTGA
 TAGATGCTCTGCAGATTGACTTCGCCAGCCCCAGCATTCACACGCTCAGGAGATTCAAGCCCCACATGCCGCTCTACCC
 TCCTGGCAAACATAAGCTCCTGCAAGGAGATCCTGGAGATTCAAGCCCCACATGCCGCTCTACCGATCTCAGG
 TTGACCCCTCCTACCACCAACATGCAGCGCTCAAGGCCCTCACCACGGCTCACTGCCAACCTTATTGATGCTG
 GTAGTAACCTGCCAGGCCACGCCATAGTGGAAAGACAATCTATTAAAGCAGCTCACCACTGCAGGAAGGGTGTAG
 TCTCATGGGAGATGATACTGGAAAGACCTTCCCTGGTGTCTTCTCAAAGCTTCTTCCATCCTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCACCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTCCTGGGTGTGGACCACGTGGCCACAAGCATGCCCTACCACCCGTAATGGCCA
 AGAAACATTAGCCAGATGGACCAGGTGATCCAGGGACTGTGGAGCGTCTGGAGAAATGACACACTGCTGGTAGTGG
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 TCTCCAAGGCCTCTGCTGACTACCAGTGGCTCTCCAGAGGCCAACGGGCTGAGGCACACTGCCGACTGTGA
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 GCATGGCGGGGGTACTGCTCTGGCTGCTTATCTGCCGCTGGCATCTCAGTGGCAATATCCC
 CAGGCTTCCATTGCCCCCTACTCCTGACACCTGTGGCCTGGGCTGGTGGGGCCATAGCGTATGCTGGAC
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 TTGCTGGAAAGCCTGGCTGGCTGGGGTCCAAGAGGCCCTGGCAACCCCTGTTCCATCCCTGGGCCGTCC
 TGTACTCCTGCTGTTGCTGGCTGTGTTCTCTGATAGTTGTTGAGCTGAGGCCAGGGCACCCCT
 TCCCTTGGGCTCATTCATCCTGCTCTGGTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAC
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 CGGGCCTGGTGGCCCTGTTAGCTGCCGTGGCTGTGGCTGGCCATGGTAAATCTCAAGAGCCCCGAGGCCAC
 CCATGCTCTTGTGCGCTGGGACTGCCCTAATGGCATTGGTACTGCTGCCTACTGGCATTGGCCTGGGG
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 TGGCTGCTCAGGGCTCGCGCTGCTGCTCTGGAGCCTGTGACAGTGTGGTAAGGCTGGGAGGGCCTCCAA
 GGACCAGGACTGTCCTCACTCCCTCTCAGGCCCCCACTTCTCAAGCTGACTGGATTATGTGGTCCCTCAA
 TCTACCGACACATGCAGGAGGAGTCCGGGGCGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG
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 CCCCAGGGAAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGGCCACTGATGGAGATGCCGCTCCGG
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 TGGGCTGTGCCCTGGCAGCTCCATCTCGCAGGCATCTCATGGCTGGAAAGTGTGTTGCCCTAAGTT
 TTGAGGCTGTGGCTCAGGAGCTATTCTGGCCAGCAGGAGGTGAGCTGAGAGTGGATGGT
 CTGTGAGCTCTGGCTCAGGAGCTATTCTGGCCAGCAGGAGGTGAGCTGAGAGTGGATGGT
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCTGTACAGGACTGAGCTGAGAGTGGATGGT
 TCTACTATCATGCAGCAGGGCCGCTGACATCTAGGACTTCAATTCTATAATT
 TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGTCTCGAAGTGGAAATAAA
 AGGCCGGCGTGGGTGACTTGCACCTATAATCCCAGCACTTGGGAGGCAGAGGTGGGAGGATTGCTGGT
 AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

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VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEPM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAAGWGSKRPLATLFPIPGPVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVQLHWEQQLLPPKLLTMRPLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWAAFVGFPFGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKQQPPGNEADARVREEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT
 GTCTCTGGTGGTTGCCTAAACCTGCAAACATCACCTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTACTGCCTG
 ACACGTGGAGTCCTCGTCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTG
 CCCATATCTATTACCGTGTTCTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTTGATTTATGGAAATGAATTGACAAAA
 GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACTTATCACCCCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTAG
 GGTATGCTTCGCATTGATGGAAATTGGACTCTGAAGAAAACACGGAAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAAGAACACTGACATTGTCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACTGGCAGGCTGTGATTCCCTCGCTGTCAGCTCGACCAGGATTAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGGT
 TATATGTGCAGATGGAAAACTGATGCCAACACTCCTTGCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGATGAAAGAAGTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTCAAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQ
CARTLKQDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIGNEFD
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTIQLLESQAALAVLGQTLQSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDSLGEGLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
 TCTGCC**ATG**GGGCTCGGGTTGAGGGCTGGGACGTCCCTGCTGACTGTGCCACGCCCT
 GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG
 TGACCCCCCACTCCAGGCCATACATGGCATCCGTGCGCTTCGGGGCCAACATCACTGCGGA
 GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTGCTGGCGCCACGTCCCTGAGTACTGCGGAGCCCACCCAGCAGG
 TGTTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGCTGGCCCTGCAGTGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCAGGCCACAGCGGGGACACGGTGCCGGTGGCTGGCTGGGCT
 TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCAAGGTCCGAGTGCTGGAC
 CCGGACGCTGCAACAGCTCTGGAAGGGCACCTGACACTTACCATGCTCTGCACCCGAG
 TGGGGACAGCCACAGACGGGCTTCTGCTGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCCTGTTCTCCTCGGCCCTGGTGC GGACCCCCAAGACCCCCGAC
 GTGTACACGCAGGTGTCCGCCCTGGATCTGGACGTGGTTCGGCGAGCAGTCC
 CCAGCCCAGGCCCTGCCTGGGACCACCAGGCCAGGAGAAGCCGCC**TGA**GCCACAACCT
 TGCAGCATGAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCACGGG
 AAGCCTGATGTTAGGGTTGGGTGGGACGGGAGCGGTGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAGVLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWC GDPKTPDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCACTCCGGACGCCCTGACGCCCTGA
 CGCCTGTCCCCGGCCCGGCAATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGCTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATGGGAAGCAGACCGCCTT
 GGAACCTGCCAGGAGAGGAGGCAACATCATCCTGCCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
 TTGGCTCCCTCAAGTCTATCCGAGAGTTGCAAAAGATCATGAAAGAGGAGGAGCGAGT
 GGACATTCTAACAAACGCGGGTGTGATGCCGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTGGCGTTAACCAACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGCCCATGTTGCTGG
 GCACATAGACTTGTGACGACTTGAACACTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTGCCATCGTCCCTTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT
 GGTGTACTGTCAACGCCCTGCACCCGGTGGCCAGGACAGAGCTGGCAGACACACGGG
 CATCCATGGCTCCACCTCTCCAGCACACACTGGGCCATCTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACTGGCCGTGGCGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCGGAGGCTTGGCTGAAAGTGCCCGCTGGTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGATAACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGCCCATGCCAGCTCCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCATGCCAGTAGGTTCTAGGGGGCGTGGCCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCGGCTGGCTGGTCTGCTCTGCTGCCAGCAGGGAG
 AGGGGCCATCTGATGCTTCCCTGGAAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC
 TGTGCACTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGAGGGTCCAAGGTGC
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGGTCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTCCGTGCCAGAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGAAACCCACCAGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKLKASAPSRIIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTE
SSTTLGPIFWLLVKSPELAAQPSTYLVAAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATGTGGT**CCTGGGCGCGGCTGGCGGCCTGCTGGCGGTGCTG
 GCGCTCGGCACAGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGCGCTGAC
 CAGCGTGGCGCGCCCTGGCGCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCAGTACCTGC
 GCAGGGGAGGAGGCGCGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTCTTGCA
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTTCATTTACTCTCATCAAACGCCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCAGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTT
 TCAGAGAGTCAGTGGCTTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTCTCTCA
 CAGGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTCCGAGGATCTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCCTGGATCACTGGCTTGTCTTATTCGGCCAGGAA
 ATGTTCTGTGCCCTAGCCTCTCGGAGTTCTCTACAGCCCAGATAATAAGAGG
 ATGCCAGGAATGTCTTGAATATGAAAGGCTTTGGCAGAGAGCCCCAACCACGTGGTAGC
 TGAGGCTGTCATCCAGAGGCCAATATACCCACCTGCAGACCAGAGCACCTACGAGGGC
 TATGTCAGACCCCTGGGTTCCAGCCCACCTCTACCCAGATCCCTAGCCTCTACTGTTCTAT
 GAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCATCCGAAGGAGGTCATCCACCTGG
 GCCCTACATTGCTCTACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGGCATCAGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAACTGGTGACCCCTAA
 CCACCGCATTGCTGCCCTCACAGGCCCTGATGTCGGGCTCCCTATGCAAGAGTATCTGCAGG
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTGGTGGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCGAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
 TGGTGGAGTCTGTGGCTTCCAGAGAACGCCAGGAGCCAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGAGAACAGGCCCTGTCAGCTTGTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTGTTACCAAGGGACACTGAGAATGTACATTGATCTGCCCAAGGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAAGTTCTGG
 AGTTCAAGATACTCTGTTGGAACAGGAACAGGACATCTAACAGTCAGGTCGATCAGTGGGTC
 TTTGGCACTTGAACCTTGACCAACAGGGACCAAGAACAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACTTAACAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCAGAACGCATATCCAGATGAGTGGTACATTATATAAGGATTTT
 TTTAACAGTGAACAAACTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA
 ATGTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSLVARALAPERRLLGLLRRLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHQLQTRDTYEGLCQTLGS
QPTLYQIPSILYCSYETNSNAYLLLQPIRKEVHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSCTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGTTAACGTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGAG
 CGCCCAGGATGCCCGCGGGGACTCGGAGCAGGTGCCTACTGCGCGCGCTCTCCTACCTC
 TGGCTCAAGTTTCACTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCT
 GTCTGTGGCATCTATGCAGAGGTTGAGCAGAAATAAAAACCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTGGCGTCGTATGTCATGGTCTCCTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTGATACATCCTGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCCTGAACGACAACATTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAACATCAGTACCGACTGCAGTGCAGTGCCTGGACCCCTGGCCTGTGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCACACCATGTGTGGCTACAAACTATCGAC
 AAGGAGCGTTCACTGTGCAGGATGTCATCTACGTGCAGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCTGGCATCCTGCTTCCCCAGT
 TCCTGGGGTGCCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCAATAGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGCCCTGCCTC
 CCCAGGGAGCAGGCCTGGCCTCCCTAACAGGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCCTTCTCCAGGCCTGGCTACAGGGAGGG
 GAGCCTGAGGCCTGCTCAGGCCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCCCTGGCGAGGAGGAAGG
 GCATCTGGGAAGGGCAGGAGGGAAAGAGCTGTCCATGCAGCCACGCCATGCCAGGTTGGC
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGCAGGGCGCTGCTTCCTTGAGCCTA
 GTTTTTTACGTGATTTGTAACATTCTTGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCCGATGTCTTATTCTGCCCTCCCCAACCAGTTGTTAA
 TCAAACAATAAAACATGTTGTTGTTAAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIVYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMEIGGVVALTFRNQTIDFL
NDNIRRGHENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCGGGCCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACTGCTGTATAAGCTCTCCTCTGGTAACGCCCTAGCTAACG
 AGGTCACTGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAAACAGCTGTGTCCCCTG
 ATCGAGGCTTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTGACACCATT
 AGCTCTACCTGGGGCCAAGTTGGACTCACAGGAAAGGTGACCAAGTGGTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCAACCCCTGGACAACATCCCCTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTGATGGTCCCTGTTGG
 ACTCTGTGCTTCCTGAGAGTGCACCGTGAAGTCAAGCATGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAACTGATCGTGTGGAAGTGTTCCCTCCA
 GTGAAGGCCCTCCGCCCTTGTCACCTGGCATCGAACGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTCAATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
 AGCCTCCTGTGGAAACCCAGCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGI PVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSH GSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFFNNSAASLTMP TLNDNIPFSLIVSQDVFKA AVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRS GVPVSLVKALGFEEAESSLT KDALVLT PASLWKPS SPV S Q
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATGGCAGCGCGTTGGCGGTTTGGTGTCTCTGTGACCATGGTGGTGGCGCTG**
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTCCCGTCGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAC TGCA TAGACAGTGTGTCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACTCCTGGCGATACTCCAGTGATTACCAACAGGATATTTGCCATGGTGGATTTG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTCACTGAGCTTACAGGTGCGGGGTTTCAGC
 CCTGCAAAAGGAAACCAAACGGGGTGTACATATGAGTTACAGGTGCGGGGTTTCAGC
 TGAGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCCTATGTTGGGATTGCTTTGGCTTTATTGGTGGACTTGTGTAT
 CTTCGAAGAAGTAATATGGAATTCTCTTTAATAAAACTGGATGGCTTTGCAGCTTGTG
 TTTTGTGCTTGTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCCACGGGACATGTGAATTATATCCATGGAAGCAGTCAGGCCAGTTGTA
 GCTGAAACACACATTGTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTCTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTCAGTGGATGCTCTATTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAAA**AGGTCCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTAAATAGTTAATCATTAAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTAAAATCTGAGGTATTGAAAATAATTATCCTCTTAACCTCTT
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTAAAAATTGAAAA
 CTACTACTTGTAGTTAGAACAAAGCTAAAACACTTTAGTTAACTGGTCATCTGAT
 TTTATATTGCCTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCACTTCTAGCTTCTCATCTTGTGTGGATGTGTAT
 ACTTTACGCATCTTCCTTTGAGTAGAGAAAATTATGTGTGTCTGTGGCTTCTGAAAATG
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTCTCCTCCT
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTAGGTGTTAACTACCTGTATTAGAAA
 GATTTCAGATTCCATCTCCTAGTTCTTAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAATCAGTGTAACTTACATGGCCTAAATGTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTGAGACCATCTGGCCAACATGGTGAACCCCCGTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACTCAGGAGATGGAGGTTCACTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKSQLMEWTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPGRDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSF DGRLT FHPGSQVVKLPF INF
MKTRGTSFLNAYTNSPICCP SRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDV MERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLI RNRTKVRV MERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHPYPS PSSGENFGSSTFHTSLY WLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVS NVVSLVDIYPTMLDIAGIPL
PQNLSGY SLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELNVAVKFPEITYSLDQKLHSIIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMN PRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

FIGURE 77

TOP 100% IDENTICAL

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACT
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
 ATCCTTGGAGGCCTCTGGATTCAATTCTGTCCTGGAATCTTCATGGATCCTACGGGA
 CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTTTACTTGG
 GCATTATTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACTAACGATGCCTACCAAGCCAACCTCTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAAGGGGCCAGAGCTGGGGGTGGCTGGTCTGTAAAAAACAGTGGACAG
 CACCCCGAGGGGCCACAGGTGAGGGACACTACCACTGGATCGTCAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCTC
 CCCTGCCCTAACGTCCCCAACCTCAACTTGAAACCCATTCCCTAACGCCAGGACTCAGAGG
 ATCCCTTGCCTCTGGTTACCTGGACTCCATCCAAACCCACTAACATCACATCCACTG
 ACTGACCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTATTGCTGG
 GGATGGGAAGGAGAACGAGTGGCTTGTGGGCTTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
 AGACTAATTGTGCATGAACTGAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAQAMMVTSAASSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTCGCCAGAATCTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTCAGGGAAAGTCATCGCTCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGTTGAGCTCTGCTGTCTGATTCCCTTGGCCTCACAAACGATTTGTTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTCCC**TGA**GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTATATGTGTACCACTAGAGAAGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~P~~REVIAPAGSEPWL~~C~~QPAPRCGD~~KI~~YNPLEQCCYND~~A~~IVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND~~F~~VV~~K~~LKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCGTGCGCCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTAAGCTGATAAACAGAACTGCGA
CTCAGCCGGACCTCGGATGACAGGCTTGTGCGAGTCAGC**TAAT**GGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTGGGCCAGAGAACACACACTCAAUTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGCCAACATCAACCCGGCACCAACCCAAGGCTGGCTGGGAACCCCTCACCC
TCTGTGAGATTTCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWTFMVK LINQNCD SARTSDDR LCRSVS

Signal peptide:

amino acids 1-24

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWTFMVK LINQNCD SARTSDDR LCRSVS

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCCTGGGGCCGCCGCAGCGCTACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCCGCCGGCGTCCCAGCCGCTCCCGGCACCAGAAGTTCCCTCT
 GCGCGTCCGACGGCGACTGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTTCGCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
 CACGCCGTATTCCTGTATGTCTGTCCCAGGGCAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGCACGATGTGACCTTACAAGACGTGGTACCGCAGCTCGAGG
 GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCACGTTCCAGGACCTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
 CCATGGTGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACGTGTGGTGT
 ACCCATCCTCCCTCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGCAGGATGGACAGAACATTCAAGGGATTGAAAACC
 CGGGCTTGAAGCCTCACCACTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTCCATCCCTGGACCCCTGTCCCTGACT
 CTCCAAACTTGAGGTACTAGCCCAGCTGGGGACAGTGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTGAGCCAGGGCTGGCTGTGAGTGGCTCCTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGTGCTGAG
 ATTCTCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTCTGAGACATGAGCCTGGATGTGGCA
 GCATCAGTGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCCTGGCTCCCCGTTGCCAGGTGCTCTCTGTC
 AGACTTCCTTTGTACCACAGTGGCTCTGGGCCAGGCCTGCCACTGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGCTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCAGACGGGAAGTAC
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCACTGGAGATGGTGCTGAGGGAGGTGGTGGGCCCTCTGGAAAGGTGA
 GTGGAGAGGGCACCTGCCCTCCCCATCCCTACTCCACTGCTCAGCGCAGGCC
 ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGCAGGGAT
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVOTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLLDGLYCCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCPLLLLKVQKQRAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPAKEVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACCGCGTCCGCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT
 TTCCCCCGTTCTCTTCCACCTTCTCTTCCCACCTAGACCTCCCTGCCTCC
 TTTCCCTGCCAACCGCTGCTCCTGGCCCTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCCTCGTCTCCCTCCGA
 CTCCGCTCCC GGACCAGCGGCCTGACCCTGGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCTCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCAAGTGTGGAACCTCACACTCCCTCTGGACTCCGGCCCCACCAAAGTCCTGCC
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCTGAGCTGTTCCCTCC
 CGCCTGCCAACCAACCAGTGTGCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGAGGCCGGCACCCAGC
 CCCCACCTGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCCCTGAAGGAGAAACATAAGAAAGCCTGTGCATGGCGGG
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCGAGGTGCTCCAAGGCACCGGGCGGGCCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCTGGAACACCGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAAGAAGTTGCATTACCTCAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELPSPRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGT PAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGGGCCTCCGCTGGCTGTGCAGGC GGCAATGGATT CTTGC GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACCGCCTCCTCGTTATCGTACCCCGGGAG
AGCGGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG
GC GGGCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTGGCGGCGAAGGCGGCCAGCGGGAGGTACCGT
GAGACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGGCCAGCGGAGAGTCGGACCGAGATAACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAAACCCCTGGACTGACTGCTTAAGGT
CCGCAAGGC GGGCCAGGGCCAGACGCGAGTCGGATGTGGTGAAGTGAACCAATAAAA
TCATGTTCCCTCAAAAAAAAAAAAAAAA
AAAAAAAAAAA

FIGURE 88

MDSLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLIA
TLQEAAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTTCTACTCTGGCACCACTCTCCAGGCTGCC**AT**GGGCCAGCACC
 CCTCTCCTCATCTTGTTCCTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGCCAGTGCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCCAGTCAAGAACAAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCAGGAGGCACTCAGAACTGAGGCCACACCACCTCCGGAGAGTGG
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAAGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCAGCTGGCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGACACAGAACATGACACAGCCTTGTCTCCCAGGCTGCGTACTCACCTT
 GCCATGGCTGCCCGAAAGCTTCCGAGTCCGGTGCCCTCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC
 ACTTGTGTCTGCCAACAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
 TGTCCCAGAGAGAACATGCTGAGGCTGCCTTGTATCTGTGGGACCTCTATGCGTCTATAA
 CACCCGTCCTGCCAGTGGGCCGCATCCAGTGCTCCTTGATGCCAGCGCACCTGACCC
 CTGAACGGGCAGCACTCCCTATTTCCCCCAGATATGGTGCCTATGCCAGCCTCCGCTAT
 AACCCCCGAGAACGCCAGCTATGCCCTGGATGATGGTACCAAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTGTTTGATCTTCTCACTC
 CCATACATTTATATTATATCCCCACTAAATTTCTTGTCTCATTCTCAAATGTGGCCAG
 TTGTGGCTCAAATCCTCTATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTT
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGGCCAGAGTCAAAACCCCTCAATG
 TTCCCTCCTGCTCTCCTGCCCATGTCACAAATTCAAGGCTAACGGATGCCAGACCCAGG
 GCTCTAACCTTGTATGCCAGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTG
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCTCTCCTCACTCCTCCCT
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCAATTAAA
 AGGAAAATCCACAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKKGKR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAEAASFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCCGT
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCCAGTTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTCCATCACGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCGGCCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATACTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAAATACTCTGCTGTGGCTATTTTG
 GCATTGTTGGACTGAAGATTTCTTCTCAAATTCCAGTGGAAAATCCAGGCGGAATGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGCT
 TCTCAGAGTTCCAAGCAGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCG
 ATCATGGGTACTGGTCCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAATAGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTCTTCAACATAATGACCAGTCCCTTATTATACCCGTACATGCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTCTTAGGGATATTAAGGTCTCTCCCA
 GATCCAAAGTCCGCAGCAGCCGCCAAGGTGGCTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGGAAAGAAGGCTGACATTACATT
 AGTTTGTCTCACTCCATCTGGCTAAGTGATCTGAAATACCACTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTGTTCAATTACACTTCAAGTA
 AAAAAA

FIGURE 92

MALMLSLVSLLKLGSGQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWEIQLQVSALGSVPPLISITGYVDRDIQLLCQSSGFPRPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAEQELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
PDHGYWVLRLNGEHLYFTLNPRFISVFPPRKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCATGGTGCAGCCGGTGGCGGGCGGTTGCAGGGCTTCCTGGTCGGATTGCA
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGGCGAGCCGAGCGC
CATAGGGAGCCTGCCAGCCTGGCGGGGAATGTCACCGGTGGCGCGGGGCCGCGGGCAGGGT
GACCGCTGCCGGCCCCGGTTGCAGGGCAGCCACCCCTCCCTAGGGCGACGGC
TCCCACGGCCAGGCCCCGAGGACCAGGGCCCCCGCGGCCACCGTCCACCGAACCCCTGGCTG
CGACTCTCCAGCCCAGTCCCCGGAGGACCACCCCTCTTGCGACTGCTGGACCCCTTCC
ACCACCTTCAGGCGCCGCTCGGCCCCCTGCCGACCACCCCTCCGGCGCGGAACGCACTTC
GACCACCTCTCAGGCGCCGACCAGACCCCGCGGCCGACCACCCCTTCGACGACCACGGCCGG
CGCCGACCACCCCTGTAGCGACCACCGTACCGGCCACGACTCCCCGGACCCGACCCCC
GATCTCCCCAGCAGCACAGCAGCGTCCCCACCCACCTGCCACCGAGGCCCCCTC
TTCGCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
GCAACCAGACCACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGCTTACTGTGAAC
TGCAAAGAGGGCTTTACCTAAATTACACTCTGGGCTCTGTCAAGCATGTGACTGTAGTCC
ACATGGAGCTCTCAGCATAACCGTCAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTATT
TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAAACAAAG
GAGGATGAGGGCATAGATTACAAAATTTATATACTTTATTCTTACTTTATATGT
TATATTAAATGTCAGGATTAAAAACATCTAATTACTGATTAGTTCTCAAAAGCACTAG
AGTCGCCAATTTCCTGGATAATTCTGTAAATTCTAGGGAAAAATTATTGAAGAAT
AAATCTGCTTCTGGAAAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTCTT
ATGTTATTAAATACCATGGAGTTGAGGAATTGTTGGTTATTCTCTCTA
ATCAAAATTCTACATTGTTCTTGACATCTAAAGCTAACCTGGGGTACCTAATT
TTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG
TAGATTAAGCAGGAATTCTTAAACTATTATGTTGGAGGTAATTAAATCTAGTGG
ATAATGTAAGTGTATTCTAACGATTGCCCTGTACTGCACTGAAAGTAATTATTCTTGACCT
TATGTGAGGCACCTGGCTTTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT
AATGAAAAAAATAATGACAGGTTAACTCAGTGTAACTGGTATAACCCAAGATCTGCTGC
CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTTGTCTCAAG
GTTGTTGAAGATTAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA
TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAGA
ACTTTAGCTCCTGACAAAGAAGTGTATTACTTAGCACTAAATTAAATGCTTAA
TAAATGATATTATACTGTTATGGAATTGTTGATCATATTGTTATTAAATGTTAGAAG
AGGCTGGCGCGGTGGCTCACGCCGTAACTCTAGCACTTGGGAGGCCAGGGGGTGGAT
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCGTCTACTAAA
AAATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGAGTCCCAGCTACTCGGGAGGCT
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
GCACCTCCAGCCTGGTGAAGAGAGGGAGACTCTGTTAAATTTAAATGCTTAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTLSTTGPAAPTPVATTVPAPTPRTPTDLPSSNSVLPTEAPS
SPPPEYVCNCVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGC GGCG CAGT GTAG ACCT GGGAGG **ATGG** CGGC CTGCT GCTGGCTGCTTTCTGGCTTG
TCTC GGGT GCCCAGGGCC CAGGCCGTGTGGTGGAAAGACTGGACCC TGAGCAGCTTCTGG
CCCTGGTACGTGCTTGC GGCTCCCGGGAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGT GACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGGC GTGCTGGAGCTCTGGGTGCTGGCCACCAACTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGACGAGCCCTAACACCGTGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGCTTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTACAG **TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAGCTCAGAATAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTLTPEPNLRTLSSQHGLGGCDQSVMIDLICKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQLEFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSO

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGGGCCCTGGCACCTCTAACCCCAGAC**ATG**CTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGCAGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTACCCCTCGCAT
 GGCTGGATTTACCCTGCCAGTAGTCATGGCTACTGGTCCGGAAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCAAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCC TGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACAC
 CCGCTCCTCGGTGCTCACCTCATCCCACAGGCCAGGACCATGGCACCCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCC
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCGTGACCTGTGCC
 TCACAGCCCTCAAACCCGGGGTGTGGAGCTGCCCTGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTGGCTCTCAGCAGGTCTACCTGAACGTCTCC
 AGAGCAAAGCCACATCAGGAGTGAUTCAGGGGGTGGTGGGGAGCTGGAGGCCACAGCCTG
 GTCTTCTGTCCTCTGCGTCATCTCGTTGAGGTCTGCAGGAAGAAATGGCAAG
 GCCAGCAGCGGGCGTGGAGATACGGCATAGAGGATGCAAACGCTGTCAGGGTTGAC
 CTCAGGGCCCTGACTGAACCTGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCGCTCCTCAGTGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTCCAGATGG
 GAAGCCTGGACTCGGGGGACAGGAGGCCACTGACACCGAGTACTGGAGATCAAGATCC
 ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGG
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAAC
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGTTAGAGTCAGGAAAGTATCTCAAAC
 CCACACTGTGCCCTCCCTTATTAACTAAAAGACAGACAAATTCTCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTL SIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNSSLSLPEGQLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVR
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCGTTCCTGGTCA
GCTCGGCCTGGCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGAAAGTTGGAAGGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCCGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTACTGCAAAGACCAGCACCAGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCCTCCGAACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACCAAGACACAGAGCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCCTCCCTGCTCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCCAAAAAAAAAAAAAAA

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

Top sequence

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGCCCGCTCCTCCCCCTCCAGGCC **ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTGTAGGGGGAGAGACCAGGATCATCAAGGGTCGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCAGTGGCACCAGCTGCCTCATTCCGGCTGGGCAGCACGTCC
 AGCCCCAGTTACGCCCTGCCTCACACCTGCGATGCCAACATCACCACATTGAGCACCA
 GAAGTGTGAGAACGCCTACCCGGCAACATCACAGACACCAGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGAUTCCGGGGCCCTCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAAT**TAG**ACTGGACCCA
 CCCACACAGCCCATCACCCCTCATTCCACTTGGTGTGGTCTGTTCACTCTGTTAAT
 AAGAAAACCTAACGCAAGACCCCTACGAACATTCTTGGCCTGGACTACAGGAGATG
 CTGTCACCTAACGCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCCT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAH
CLKPRYIVHLGQHNLQKEEGCEQRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAIRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTCTTATTCA GATT CATT GTTT
TCTTTATCTGTGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTGCATCGTCCAGAAA ACTGCTCTAACAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCAAATGGTTGTTCTGGTGTGGCAAGTCATAAAAGGCCATA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACC GGATGCTACATTGATTTG
AGATTGAACTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGATTGAA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTTAAGA
AGAATGACCATGATGGTATGGCTCATTCTCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTGTATTCTACTTTTTTTAGCTATTACTGTACTTTATGTATA
AAACAAAGTCACTTCTCCAAGTTGTATTGCTATTCCCCTATGAGAAGATATTTGA
TCTCCCCAATACATTGATTTGGTATAATAAAATGTGAGGCTGTTGCAAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTTGCTTCTGCTGAGCCTTTGGAGCT
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCCAAATGCTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTCAAAC
CCC GTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCC TGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACCTCAGGAGGCAGAAGTTGCAGTGAAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA
TAGTTCTTGTTCATT CGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGT CATCCCCTGGT GACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCCTTCCCCAGACTTGAAGTGACCCACC**ATGG**
 GGCTCAGCATTTTGCTCCTGTGTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
 CAGCCTGCGCTGCGGGGTGTCCTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGAACACAGCCTCAGCCAGCTGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTGTGACCCATCCGGTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCCCTGCCGTCCCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGC
 ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAACATCAGGAGAACATGGTGTGCAG
 GCGGCGTCCCAGGGCAGGATGCCAGGGTATTCTGGGGCCCTGGTGTGTGGGGGA
 GTCCTCAAGGTCTGGTGTCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAAC**TGAC**
 CTGTTCCACCTCCACCCCCACCCCTTAACCTGGTACCCCTCTGCCCTCAGAGCACC
 AATATCTCCTCCATCACCTCCAGCTCCACTCTGTTGCCCTGGAACTTCTGGAACTT
 TAACTCCTGCCAGCCCTCTAAGACCCACGAGCAGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAATATAATGAAGGAGGGCAAAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLKVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGGCCACACGCAGCTAGCCGGAGCCCCGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCCGCGAAGCCTGGAGCCGGGGAGCCCCCGCCTGCC **ATG** TCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGAAGGCCTGGCTTGTGACAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
 GAGATCAACCAGGGAGTTCTGTGACAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
 GCTCACAGCCTCAAAGAGAAAGTACATGGAGTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA
 CATGATGCTGGGAAACGGTCGGCTGTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC **TGA**
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACTCCCTCCGATTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGGTTGTTGTTGTT
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGTCGGGAATCC
 TGAGCCTTGGTCCCCTCCCTCTTCTTCCCTCCCTCCGCTCCGTGAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGGCAGGGCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTTTGGGTTCCCTGGACAGTGCATGGTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTGGCATTGGAGCCCTCAAGAAGG
 TACCAGAAGGAACCCTCCAGTCCTGCTCTGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG
 GGGTTGGGGGAAAGGTAGCTCAGTGCTGTTCCACCTTGTAGGGAGGAGACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGTGACCCCAATCTGCTGAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCCTCCTGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCACACCATGGCCCCCGGGTGGGCAGGGGTGGCGCCGCGCGCC
 CGCCTGGCGCTGGCCTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCGTCGCCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGGCCTCCCGCGCGTT
 CTCGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATACCAAGGATC
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAGGT
 CAGCGTCATCGAGAGAGGGCGCCTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTCCAGAGCACGCCGAAGCTACCAGACTA
 GATTGAGTAAAACCAGATCCAGGGATCCCGAGGAAGGGTCCCGGGCATCACCAGATGT
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGATTGAAGATGGAGCCTCCGAGCGC
 TGCAGCTGGAGATCCTTACCCCAACAAACAACATCAGTCGCATCCTGGTCACCAGC
 TTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCAGCGACAGGACAGTTGCCAGTTCACACTCT
 GCATGGCTCCTGTGCATTGAGGGCTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG
 TGCCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTCGCC
 CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCA
 ACTTGCCGGAGGGCATCGCGAAATACGCCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
 GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCCAGATGCCTCCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
 AGATCACCAGAGATTGCCAAGGGACTGTTGATGGCTGGTCTCCCTACAGCTGCTCCTCCTC
 AATGCCAACAAAGATCAACTGCCTGCGGGTGAACACAGTTCAGGACCTGCAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCTGCCACTCTGCAGT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCAGTGCCTGAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGGCCG
 ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAACGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTAGCAGCGAGTGCCTCATGGACCTCGTGTGCCAGAACCTGGCA
 TGTGAGGGCACGATTGTGGACTGCTCAACCAGAACGACTGGTCCGATCCCAAGCCACCTCCC
 TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGAAACCAGCT
 GGAGACCGTGCACGGCGCGTGTCCGTGGCCTCAGTGGCCTCAAAACCTGATGCTGAGGA
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTGGCGGCTGAGTTGGTGGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCTTCACCACGCTGTCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGGGATCGTCAGTGGAACCCCTAGGTGCCAGAACCCATTTCCTC
 AAGGAGATTCCCATTCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAGT
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACCTAACAGCGTGCCTGGAGAGAGCTGTCGCCACCTGACGCT
 TATTGACCTGAGCAACAAACAGCATCAGCATGCTGACCAATTACACCTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTCAAC
 GGGCTCGGGTCCCTGCGAGTGCTAACCCCTCATGGCAATGACATTCCAGCGTCCCTGAAGG
 CTCCTCAACGACCTCACATCTTCCCCTGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGCGGGTACAAGGAGCCTGGCATCGCC
 CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCTGCTCACCACCCAAACCCACCGCTT
 CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCCTGCC

FIGURE 111B

E 9247007
T 4147007
C 12147007
G 10447007
A 10447007

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTAGCTGCTCCTGCCCTC
 TGGGCTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGAACAGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGATCAACAACATACGTGTGTATCTGTCCGCCCTAACTACAC
 AGGTGAGCTATGCGACGGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTCA
 GAGCAGTCAGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGCGAGTGTGCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGCCCTACAAGTGCCGCCACGGGCCCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGGCTTCAGTGGACCCTTCTGTG
 AACACCCCCCACCCATGGTCTACTGCAGACCAGCCCAGTGCAGACTACGAGTGC
 CAGAACGGGCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGA
 ACTGGCCTCCGCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCACTGACA
 AGGACAAACGGCATTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTAC
 ACCAGGGCCACGTGCGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGT
 ATGATGGGCAGTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCAT
 AACAGCCCCCTCTACCTTGGAGGCATCCCCACCTCCACGGGCTCTCCGCCCTGCC
 ACCGGCCTCTAGGCCTCCACGGATGCATCCATGAGGTGCGCATCAACA
 ACAGCTGCAAGGCTCCACCACAGTCCCTGGGGTGTCA
 ACCAGGCTGCAAGTCTGCACCGT
 GTGCAAGCAGGCCCTGTGCCCTCCGTGGAGAACAGGACAGCGTGGTGT
 GCGAGTGCGCCAG
 GCTGGACCAGGCCACTCTGCAGACCAGGAGGCCGGACCCCTGCCTCGGCC
 ACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGT
 CAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAACATGACTCTGCCAATGCC
 CTGCTCAGCCTCAAGTGT
 CACCATGG
 GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCC
 CTGCGCCAGCCGGCTTAGCGGC
 GAGCACTGCCAACAAAGAGAACATCCGTGCC
 TGGGACAAGACTAGTAGCC
 GAGAGGTGATCCGCC
 GAAAGGTTATGCATCATGTGCC
 ACAGCCTCCAAGGTGCC
 CATCATGGA
 ATGT
 CGTGGGGCT
 GTGCTGCC
 CAGGCC
 ACCCGC
 AGCAAGCG
 CGGAA
 ATACGT
 CTTCCAGTG
 CACG
 GACGGCTCCTCGTTGT
 TAGAAGAGGTGGAGAGACACTTAGAGTG
 CGGCTGCC
 CAGCTTG
 ATGGAGTT
 GGGACAGCC
 CTAAG
 CCCCTGCC
 GCCTGCC
 ACCTCTCG
 GACTCCAG
 CTGATGG
 GAGTT
 GGGACAG
 CC
 AGAGA
 ATATTA
 AGTAT
 ATTGT
 AAAATA
 AACAAAA
 AATAGA
 ACTTAA
 AAAAA
 AAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRN
 AERLDLDRNNITRITKMDFAGLK NLRVILHEDNQSVIERGAFQDLKQLERLRLNKNKLQVL
 PELLFQSTPKLTRLDS ENQI QGIPRKAFRGITDVKNLQLDNNHIS CIEDGAFRALRDLEIL
 TLNNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVC PAPHEPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAI PAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQ LLLLNANKINCLRVNTFQDLQNLNLLS L YDNKLQTISKGLFAPLQSIQTLHL
 AQNP FVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SEC FM DLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVS VLEATGIFKKLPN
 LRKINLSNNKI KEVREGAFDGAASVQELMLTG NQLET VHGRVFRGLS GLKTLM RSNL I SCV
 SNDTFA GLSSVRLLS L YDNRITTITPGAF TTLV S L STINLLS NPNC NC HLA WL GKW LR KRR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVT ELYLEG NHLTAVPRELSALRH LT LIDLSNN SISMLTNYTFSNM SHLSTL L
 SYNRLRCIPVHAFNGLRSLRVLT LH GNDI SSVPEGSFNDL TSLSHL ALGTNPLHCDCSLRWL
 SEWVKAGYKEPGI ARCSSPEPMADRLLLTT PTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEQQR
 CEINPDDCEDND CENNATCVDGINNYVCICPPNYTGE LCDEVIDHCVPELNLCQHEAKCIPL
 DKGFSECVPGYSGKL CETDN DDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPP MV
 LLQTSPCDQYEQNGAQ CIVVQQEPTCRCP PGFAGPRCEK LITVN FVGKDSY VELASAKVRP
 QANISLQVATDKDNGILLYKGNDPLA LE LYQGHVRLVYDSLSSP TT VY SVETVNDQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIHEVRINNE LQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSV VCECRPGWTGPLC
 DQEARDPCLGHRCHHGKVATGT SYMCKCAEGYGGDLC DNKN DSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEH CQQENPCLGQV VREVIRRQKGYASCATASKV PIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTTCTGTCT
CCGGCAGGCTTGAGG**ATG**AAGGCTGCAGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGCCCTG
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTCACTATGGCATCTTCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTGCAAGAAC
GCCCTAGGATTGCACTGAAATGTCCTGTGTCATCTGTCCCCTTCCCTCCAAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTAAGAAAATAATATTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSLITDDLTDAAICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTCGATCCACTGTCCTGTGGAGGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACCTGTACATGGCTCCC
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTTGGTGTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAACGATCCTATTTACTGTCACTCCCAGATCTGCTTCAC
 CAAGAGAGATTCTTCTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTAGTCAACAGCCAGTTCACAGCTGCTGTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCCTCATCCATCTCAAATGTCACCAG
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAACTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAAGATTGACATCCAAGATTGGGAGAGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTGGCCAGTATGTGACCTTCTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC
 TCTGGAAAGCCATGTACATGCAGTCCCCAGTCATTGCTGTTAACAGCTCTACCGATATGTTACCAAC
 CCATTGACCACAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAATTTCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAC
 TGCTGGTA**TAA**TCAAGATTGTTTAAGATCTCCATTAATGTCATTTATGGATTGTAGACC
 CAGTTTGAAACCAAAAAAGAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCCTATATACCACACCTCCGTCCACTTTCAGAAA
 AACCATGTCTTATGCTATAATCATTCAAATTGCCCAGTGTAAAGTTACAAATGTGGTG
 TCATTCCATGTTCAAGCAGAGTATTTAATTATATTCTGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTGCCTTAATTGGTTTCATAGTTAAGTGTGTATCATTCAA
 AGTTGATTAATTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTCCCAGATTCAA
 CCACCGAAGTGTTCACTGTCACTGTTAGGAAATTGTTGTCCGTCTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTAAGATAATTGTATTTGCACACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEFKLFTLVSACIPVFRLLARRKKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFVKETFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

卷之三

FIGURE 117

TOP
DOWN
REVERSE
COMPLEMENT

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTGCTGGCGTGGTGGGAGCCGTGCTTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTCAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAATCATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCAGATGGTCAC
 TTGATAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG
 CCAGTTGCATAATACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTGAAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAATTTCT
 CACTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACACTGGTAACATCATCAAGGAAAGAAGCTGGATCACTGTCTCAAAGAGAT
 ATTTAAATTTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCATTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLLVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSEHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQE VIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDMSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDELVMKTSSLGFSGTQECPELRFAYMVTVLLSVLKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGC~~GGGG~~GAGACTTCAGGAGTCGCTGTCTGAAC~~TCC~~CAGCCTCAGA
GACC~~GCC~~GC~~CC~~CTTG~~CCCC~~GAGGGC~~C~~**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGT~~CATCAC~~CTTATTCTGGTCCC~~GG~~A~~CAGCAAC~~AT
ACAGGC~~CTGC~~CTGC~~CTCAC~~GTT~~ACCCCCGAGGAGTATGACAAGCAGGACATT~~CAGCTGG
TGGCC~~CG~~CTCTGT~~CACCC~~T~~GGGC~~CT~~TTG~~CAGTGGAGCTGGCCGGTTCC~~CTCAGGA~~
GTCTCCATGTTAACAGC~~ACCCAGAGC~~CTCATCTCCATT~~GGGG~~CT~~ACTGTAGTGC~~ATCC~~GT~~
GGCC~~CTGT~~C~~CTCTTC~~ATATT~~CGAGCG~~TTGGAG~~TGC~~ACTAC~~GT~~ATT~~GGT~~ACATT~~TTGT~~
TCTGCAGT~~GCC~~TT~~CCAG~~CT~~GT~~CA~~TGAA~~ATGG~~CTTATT~~CGTCACC~~GT~~CTT~~GGG~~CTGAAA
AAGAAAC~~CC~~TT~~C~~**TGA**TTAC~~CTT~~CATGAC~~GGG~~A~~ACCTA~~AGGAC~~GAAGC~~CTACAG~~GGG~~CAAGGG
CCG~~CTT~~CGT~~ATT~~CC~~GGAA~~AGGA~~AGG~~CA~~AGG~~C~~T~~AGG~~CT~~CG~~GT~~TT~~CCC~~CT~~CG~~AA~~ACT~~GC~~TT~~
TGCTGGAGGATATGT~~GTT~~GG~~AATA~~ATTAC~~GT~~CT~~TGAGT~~CT~~GGG~~ATT~~ATCCG~~CATT~~GT~~ATT~~TA~~
GTG~~CTT~~GT~~A~~AAAA~~ATGTT~~GT~~AGTA~~AC~~ATTA~~AG~~ACTT~~AT~~ATAC~~AG~~TTT~~AG~~GGG~~ACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCTGCCGCCACTATGTCCGCCGCTCTATGCTGCTTGCCTGGCTCTCC
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCTGCTGCAGCCCCATA
GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCAGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCACTGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGCAGCCCAGGGTCTACTGGCCTGCAGGTGGCT
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTTACCAACCTCATCCAGAATTGGCACACTACCGCTCCCCCTGAGGCC
CTGCTGATCCGCACCCATTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTILGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

EFFECTS TOOT

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAGATGCAACT
 GACTCGCTGCTCGTGTTCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCAGG
 ATGATGGTCCTCCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGCCAGCCCCGGCC
 CGGGTGCCTCGGAAGCGGGCCACATCTCACCTAACGAGCCCATTGGCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACGCC
 CGAACACAGCCCCCACCTCAGCAAGGTGAAGAAAATCTTGGCTGGGCAGTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTACAGGAAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTCATCGAAGCCAAG
 GCCTCCAAAATCTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGGACCTC
 GCTTGACCCACGACCAAGATCTGCTCCAGACCACGCTCAGAGCTCAGGCCACCT
 GGAGCTGCTCCAGCCCTCAAAGTCGTGTCTACATGCCCTTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATAACCCCTACTACCCATC
 TGGGTGACCCAGGGCAGGCCACAGAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG
 CTGGTCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGCT
 CTCTGTGCAGCCTCACAGGGTTGCCACGGCACAGAGAGATGCTGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGAACAGGGAGGGGAGATTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCCTAGGAGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCCAGCCCTGCCAGTGGCGCCCTGAGCCCTTGTGCTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT
 GCTGATGGCACACCCATCCTAACGCTAACAGACAGGACGATTGTGGTCCCTCCACACTAACGGCC
 ACAGCCCATCCCGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGAG
 CATCCATGTCCGGAGAGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCAGCAGCGGGCACGGGTGGGCAGGGCCGGCCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTGTGGGTGGGGAGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPNSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQQEQQIFIIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVVCYIAFYSTDYRLVQKVPDNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGACTTCAAGGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCAGGATCCGGGTAGGAGGCGACGCCGAGCACCGGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACC**ATGGGCTCCGGCGCCGGCGTCCCGCGTGGCG**
 GCCGTGCTGCTGGTCCTCACGCTGCCGGGCTGCCGTCTGGCACAGAACGACACGGAGCC
 CATCGTGCCTGGAGGGCAAGTGTCTGGTGTGCACTCGAACCCGCCACGGACTCCAAGG
 GCTCCTCTCCCTCCCCGCTGGGATATCGTCCGGCGGCCACTCCAAGGTGCCTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCTTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTCACATTGGAGTCTGTCTTGACCAA
 GAAAAGGAATTACAGTTACAGTTACAGTTACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCAGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCTACCTAGATAAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCTTTATTGGTTCTCATGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTGAACCAATACAAAATTACAGATTATTGTG
 TGTGTCTGTTCACTATTTGGATTGGACTCTAAGCAGATAATACCTATGCTAAATGTA
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTTCATTCTGGATTACTGAATTAGT
 TACAGATGTGGAATTATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACTCTAAAGTTCTGACTTCATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATTTGTTTATTCTTGGAAATTAGTTGTTGGTTCTGTAA
 AAAACTGGATTTTTTCAGTAACGGTATTATGTTCTCTAAAATAAGGTAATGAA
 TGGCTGCCACAAATTACCTGACTACGATATCATGACATGACTCTCTCAAAAAAAA
 GAATGCTCATAGTTGTTAAATTGTATATGTGAAAGAGTCATATTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTACCTTATTGC
 TCAACTTAATTAAAATGATTGATAATAACCACTTATTAAAAACCTAAGGTTTTTT
 TCCGTAGACATGACCACCTTATTAACTGGTGGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGTTGAAGTATCATCTGGTTGCCTTAACCTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATCTAAATTAGTGAATAT
 CTTGTCTTGTAGGTCAATGAAATTCAAAATTATTATGTCTGTTAGAATAAAAGA
 TTAATATATGTAAAAAAA

FIGURE 126

MGSGRRALSAVPAPVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI
SVRAANSKVAEFSAVRSTNHEPSEMSNKTRIIYFDQILVNNGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMNLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGC
TTTCTTCTGGTTGGTGTCTACTGATTCGTCCCTGTTGGTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTC
TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTAAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCCTATGTTCTGGCT
TGGGCTTGGAAATCATGAGTGGAGTATTCCTTGTAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTGAGATTCTCCTCAATTCTCCTTATTGAGCTTCATGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGCTGGTGTAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTGCCAAG
ACAAGAACTTCTTACAACCAGCGCTCCAGA**TAA**CCTCAGGAAACCAGCACTCCCAA
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLF
GIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFDGCEKKW
GILLIVLLTHLLVSAQTFISSLYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGC**ATGTTCGCTTGGGCTGCCCTCT**
 TGGTGCCTTGGTGGCCTCGTCGAGAGCCATCTGGGGTTCTGGGCCAAGAACGTCTCGCAGAAAGACGCC
 AGTTGAGCGCACCTACGTGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGTCTCCAGGTGCCCTAATCTCGCAGGGATGTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAACGAACCTGTGTCAAGCCCCACCAAGAATGAGTCGGAGATTCACTTCTACGTGGATG
 TGTCCACCCCTGTCAACAGTCACACACATACCAAGCTCCGGTCAGCCGATGGACATTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCAATACCACAGCAGCACAGCCCCAGTACTTCAGTATGAGTTCCTGAAGGCGTGGACT
 CGGTAATTGTCAAGGTGACCTCCAACAAGGCCCTCCCTGCTCAGTCATCTCCATTCAAGGATGTGCTGTGCTG
 TCTATGACCTGGACAACAACGTAGCCTCATCGCATGTACCAAGACGATGACCAAGAAGGCCATCACCGTAC
 AGCGCAAAGACTTCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGCT
 CCCTGCCTTCTACCCCTTCAGAAGATGAACGGTCATCAAGGGCACCGCCAGAAAACCCGTCAAGTGCTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTCAGTGGGATGCTCTTGTGGTATATTCTCTCCCTTAC
 TGCTGACCGTCCTCTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGAACCCGTGCTGGTGGCATTGACCGAG
 CCTGCCAGAAGCGGTACCCCTGAGTCCTGGCTGATTCTTCCTGGCAGTCCCTTATGAGGGTTACAAC
 ATGGCTCTTGAGAATGTTCTGGATCTACGATGGTCTGGTGAACGGCTGGACTGGGACCTCTTACG
 GTTACCAAGGGCCGCTCTTGAGCTGTAGGTACTCGGCCCCAGTGGACTCCATGAGCTCTGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGACCAAGCAATACCTCTATGTCGAC
 TGGCAGGAAGGACAAGCGTCTCTGGGAAAAGTACCAAGATCTACTCTGGAACATTGCCACCATGCTGTCT
 TCTATGCCCTTCTGTGGTCAGCTGGTGAATGTCACAGGAATCAGGACATCT
 GCTACTACAACATTCTCTGCGCCACCCACTGGGAATCTCAGGCCCTCAACACATCCTCAGCAACCTGGGT
 ACATCCTGCTGGGCTGCTTCTGCTCATCATCTGCAACAGGGAGATCAACCACACCGGGCTGTCGCGCA
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAACACTTGGGCTTCTACGCCATGGCACAGCCCTGATGA
 TGGAGGGCTGCTAGTCTGCTATCATGTGCCCCAATACCAATTCCAGTTGACACATCGTTCATGT
 ACATGATGCCGGACTCTGCATGCTGAAGCTCTACAGAACGGCACCCGACATCAACGCCAGCGCTACAGTG
 CCTACGCCCTGCCATTGTCTTCTCTGCTGCTGGGCTGGCTTGGCAAAAGGGAACACGGCGTTCT
 GGATCGTCTCTCCATCATCACATCATGCCACCTGCTCTCAGCACCGAGCTCTATTACATGGGCCGGTGG
 AACTGGACTCGGGGATCTCCGCCGCATCTCCACGTGCTACACAGACTGCATCCGGCAGTGCAGCGGCC
 TCTACGTGGACCGCATGGTCTGGTCATGGGAACCGTCAACTGGTCGCTGGCTGCCTATGGGCTTATCA
 TGCGCCCAATGATTGCTCTACTTGTGGCATTGGCATCTGCAACCTGCTCTTACTTCGCTTCTACA
 TCATCATGAAGCTCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTGCTGATCGTTGCACCTCCGTGG
 GGGGCTTCGCGCTCTCTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGAGTCAGGGAGCACA
 ACCGGGACTGCATCTCTCGACTTCTTGACGACCACGACATCTGGACTTCTCTCCATGCCATGTC
 GGTCCTCTGGTGTGCTGACACTGGATGACGACCTGGACTGTGCACTGGCAGCAGGACAGCCAGGCTAG
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGCTAGCTTAGGCTTGG
 GGGACAGCCATGGGGTGGCATGGAACCTGCACTGGCTGCCAGGAGCAGGCCGCTGCCATGGGACCCCC
 AGATGTTGGCCAATTGCTGCTTCTCTCAGTGTGGGGCTCCATGGGCCCTGCTCTTGGCTCTCCATT
 GTCCCTTGTCAAGAGGAAGGATGGAAGGGACACCCCTCCCCATTCTCATGCCCTGCACTTTGCCC
 ACAATGCCCAAGGCCATTGGACCTTCTCTCCCAACTCCACTCCAGGGCCTAGTCTGGGCTGA
 ATCTCTGCTCTGTATCAGGCCCTGGCTTCTCTGGCTGCCATCAGGCCATTCCAGTCAGCC
 AGGATGGATGGGGTATGAGATTGGGGTGGCAGCTGGGCCAGACTTGGGCTGAAGGCTGCAAGGG
 CCTGGGGCAGTGCCTATTCTCTCCCTGACCTGTGCTCAGGGCTGGCTTCTAGCAATGCGCTCAG
 AGGGACTGAGGCTGAATTCAAGAGGCTCACCTCTCATCCCCTAGCTCCAGACTGATGCC
 AGCACCAGGACTGGAGGGACAAGCGCCTCACCCCTCCCTCTTCCAGGCCCTAGTCTGCC
 AGCTGGTGGCCTTCAGTGCCTGGCAGCTGCCAAGAATGTCAGGGCAAAGGAGGGATGATA
 CAGAGGTTCAAGGGCTTCAGGCCATTCCAGGAGGCTGCTCAGGGATGTGCTGTT
 CCCCTACGTGCCAGTCAGCCTCGCTAGGACCCAGGGCTGGCTCTAAGTTCCGTCAGTCTCAG
 AGTTCTGTGTTAGTCATGCACACACATGAAACCTGGAGTTACAAGAATGCCAGCTCTGG
 CCTGGCACCCTGGCTTGGATCCCCCTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGAG
 CGGGGCCCTGCTGCTTGGGATGGGAATGTGTTTCTCCAAACTGTTTATAGCTCTGCTGAAGGGCTGG
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTTGCATTCCGTTCTATGA
 ATTGTCATTCAATAAACCAACCAGACTCAAAAAAAAAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSKDAEFERTYVDEVNSELVNIYT
FNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFCPSVISIQDVLCPVYDLDNNVAFIGMYQTMTKKAITVQRKDPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVQDQGHROKTLSQLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRAALLRNDLCALECGIPKHGFLFYAMGTALM
MEGLLSACYHVCPTYNFQDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRAWKLDGIFRRILHVLYTDCIROCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLLICVCTS VVWGFA LFFFFQGLSTWQKTPAESREHNRDCILLDFDDHD IWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTGCCCAACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCTGTCTG
ACCATGGTCCCTGCCTGGCTGTTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTGAAAGTCCAGAAAACATATGGTGAAATTTCCTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAGGGGCTGAAGGCCAGATCGTGTCAAGGGACTCA
 GGCAAGGCAACTGAGGGCCATTGCTATGGATCCAGATTGGCTCCTGCTGGTACAG
 GGCCCTGGACCAGAGGAGCAGGCAGAGTACCGACTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGTCCACAGCCTGTGCTGTGACGTGAAGGATGAGAATGACCAGGTG
 CCCATTCTCAAGCCATCTACAGAGCTGGCTGAGCCGGGTACAGGCCTGGCATCCC
 CTTCCCTTCCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACAGCCTGACCAAGCCCTGGAGAGGAC
 CTACCAAGCTGTGGTACAGGTCAAGGACATGGGTGACCAAGGCCACAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCTATACCCGACCATGGCCCAGGTACACTGGAGTGGGGTGTGATGT
 GCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAATGCAGAGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCAGGCTCAG
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTATGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCGTGAACCCACAGTCAGCATCCCTGAGCTCAGTCAC
 CAGGTACTGAAGTGAATGACTGTCAGCAGAGGATGCAGATGCCCGCTCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGGTGCTCCACTCCGAGCAGGCCAGAAC
 TCCTGCTTCTGGTGTGGCATGGACCTGGCAGGCCAGAGGGTGGCTCAGCAGCACGTGT
 GAAGTCGAAGTCGCACTGACAGATATCAATGATCACGCCCTGAGTTCATCACCTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTCCGCCTCATGGATTGGCATTTGAGAGGGGAGACACA
 GAAGGGACTTTGGCTGGATTGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACGCCAGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGC
 AGCCGGCTTCTGCTGACCATCCAGCCCTCGACCCATCAGCCGAACCTCAGGTCT
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGACACCTACACGGTGTGTTGGAGGCCAGGA
 TACAGCCCTGACTCTGCCCTGTGCCCTCCAAATACCTCTGCACACCCGCCAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC
 TTCACCCCTGGTCCAACCCACGGTGCAACGGATTGGCGCCTCCAGACTCTCAATGGTC
 CCATGCCTACCTCACCTGGCCCTGCATTGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTCAAGCCACAATGCCAGATGTGGCAGCTCTGGTGTGAGTGATCGTGTGCGCTGCAAC
 GTGGAGGGCAGTGCATGCGCAAGGTGGCCGCATGAAGGGCATGCCACGAAGCTGTGGC
 AGTGGGCATCCTGTAGGCACCCGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC
 ACTGGACCATGTCAAGGAAGAAGGCCGATCAACCAGCAGACAGCGTGCCTGAAGGCG
 ACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGAGCTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCACCCAAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCTCCAT
 CTGCCCTGGGTGGAGGCACCATCACCATCACCGAGCATGTCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGAGTGCTCAAATGTCAGGGTGTGTTGCCAATAATAAGCCCCA
 GAGAACTGGCTGGCCCTATGGGAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE
 NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPPLEHVLVMMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
 VVYQLSPEPEDGVGRAFQVDPTSGSVTLGVPLLAGQNI LLLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAAPSHEVVVVVQSVAKLVGPGPGPATATTVLVERV
 MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKFSGEVHTA
 QSLQGAQPGDTYTTLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGP NPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQM WQLLRVVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFT HWTMSRK DPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CGGGGGAC**ATG**AGGTGGATACTGTTCATGGGCCCTATTGGGTCCAGCATTGTGGCCAA
 GAAAAATTGGGGACCAAGTGGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGAAATCTCCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCCTGTCACTGCAGGCATTAAATCCTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGCAGTAATAACTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTACACAGATGGACAACATTGCCGCAGACTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCGATGTATGTAAGTT
 CAGCACTGGAAAGGCGTGGAGGCCGCGTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACAGAGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCCTGTTGCCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACACTGAAACCGATTATGGAGGAAGACGCGGTCCCAGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTGCTCGAAGTGTACCATGGACCCACGCCAATTGGAAGTGG
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGGAATTCAAGGGCTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCAGGCCAAAGCTCTGGCTCTGTGTCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATGACTGG
 CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACT**TAG**GCGATGGCTCTGCTCTGTCTACATT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTCCTACCTGTGAG
 TCAGAGCCCTGGGTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGCGGTGTCCTGCAAGAACACTGGTCTGCCAGCCTGCTCAATTGGTCTG
 CTGTTTTGATGAGCCTTTGTCGTTCTCCCTCACCGCTGGCTGGCGGCTGCACTC
 AGCATCACCCTTCCTGGGTTGGCATGTCCTCTACCTCATTTAGAACAAAGAACATC
 TGAGATGATTCTCTACCCCATCACATCTAGCCAAGCCAGTGACCTGCTCTGGTGGCACT
 GTGGGAGACACCAACTGTCTTAGGTGGGCTCAAAGATGATGTAGAATTCCCTTAATT
 TCGCAGTCTCCTGGAAAATATTCCCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCCCTCCCTCCTGTTTTTTTGAGACAGAGTTGCTCTGTTG
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACAACCTCTGCCCTGGGTTCAAGCA
 ATTCTCCTGCCTCAGCCTCTGAGTAGCTGGTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTTGTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCCCTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCTCTGGCTGAATACAAAGTAGAAGATCACTTCCTCAC
 TGTGCTGAGAATTCTAGATACTACAGTTCTACTCCTCTCCCTTGTATTCACTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCAGTGAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAAGGATGGTGAATATCCCCATCTGCTTAATGGGCTTACCTCCT
 CTTTGCCTTTGAACTCACTCAAAGATCTAGGCCTCATCTACAGGCCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGTCGTTGGTGTGTTGGTGTG
 TCCTTGTGTCCTGGTTGTGTCGTTGGTGTGTCGTTGGTGTGTTGGTGTG
 TCTGTCTATTGTATCTGGACCAAGTCCTAAGTAGAGCAAGAATTCAACCAGCT
 GCCTCTGTTCAATTCACTCAGCACGTACCATCTGCTCTTGTGTTGGTGTGTTGGT
 TTGTTTTTGCTTTACCAAACATGTCTGAAATCTAACCTCCTGCCAGGATTGTACA
 GCATCTGGTGTGCTTATAAGCCAATAAAATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFQGDQVLRINVNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIPTAAETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASLYGVLFAGVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFSPVSVSTSIAMLSQLGAHSVTKTQILQQLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
 CCTTATCTCTCACCTCAAGTCCCCTTCTCAAGAATCCTCTGTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAG**ATG**AAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTGGTCTACTATTGCATTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGTCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
 GCGTGAACCTCCAATGGGGTCAGCATACTGAGTCCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGATCAGCATA
 GCCACCAA
 CTCTGAGTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCAGCAGTGCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAA
 ACCTCCA
 GTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCAACTCTGAGTCCAG
 ACCAAGCAGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCAGCACAGC
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGCACAGC
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCC
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGTGAGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAA
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAATTCCATAGTCATCTACTGCAGTGAGTGAGGCAA
 AGCCTGGTGGTCCCTGGTGCCTGGAAATCTTCCTCATCACCCCTGGTCTCGGTTGTGGCG
 GCCGTGGGCTCTTGCTGGCTCTTCTGTGAGAAACAGCCTGTCCTGAGAAACAC
 CTTAACACAGCTGTCTACCACCCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCTAACTGGTTCTGGAGGGAGACCAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC**TGA**GCAGCCCCGGAAAGCAAG
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGGCACCAAGACCTGGTTCTCATTTCATC
 CCAGGAGACCCCTCCAGCTTGTGAGATCCTGAAAATCTGAGAAGGTATTCTCACC
 TTTCTGCCTTACCAAGACACTGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCAACACACGACAAAGAGAAGCTGTGCTGCCCCGGGTGGGTATCTAG
 CTCTGAGATGAACTCAGTTATAGGAGAAACCTCCATGCTGGACTCCATGGCATTAAAA
 TCTCCACAGTAAACAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

MKMQGNVLLMFGLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATI
SGSSVTSNGSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHPRPRWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTCCGACCTTC
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGGCC
CTGTCGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATAACAGTGGAAATCACGC
ATGCCGGAAGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGCCACACCGGC
AAGGAGTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGTCCAAGGGTTCCACACTGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACCTGCTGAATGGC
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGTTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTG
GGATTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKFVNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGCGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGG
CCCGCGGGGGCGATGACCGTGCCTGACCTGACTCACTCCAGGTCGGAGGGGCCGGGGCCGGGGCGACTCG
GGGGCGGACCGCGGGCGGAGCTGCCGCCGTGAGTCGGCCGAGCCACCTGAGCCGAGCCGGGACACCGTC
GCTCCTGCTCTCGAATGCTGCGCACCGCGATGGCCTGAGGAGCTGGCTGCCGCCCATGGGCGCGCTGCC
CCTCGGCCACCGCTGCTGCTCCTGCTGCTGCTGCCCTGCTGCCAGCCGCGCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCCAAC
ACAGCCCTCTGCTGAGCAGGGATGCCAGGACCTGTACGTGGGTGCTGAGAGGCCCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCCAGGGGGAGTACCAAGGAGCTGCTTGGGTGCAAGACGAGAAGAAACAGCAGTG
AGCTCAAGGGCAAGGACCCACAGCGCAGTGTCAAAACTACATCAAGATCCTCCTGCCGCTCAGCGGAGTC
CTGTTCACCTGTGGCACAGCAGCCTCAGCCCCATGTGTAACCTACATCAACATGGAGAACTCACCCTGGCAAGG
GACGAGAAGGGATGTCCTCTGGAAGATGGAAGGGCCGGTGTCCCTGACCCGAATTCAAGTCCACTGCC
CTGGTGGTTGATGGCAGCTACACTGGAACAGTCAGCAGCTCCAAGGGATGACCCGCCATCTCGGGAGC
CAAAGCCTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTGCCCTCAGCCTAC
ATTCTGAGAGCCTGGCGAGCTTGCAAGGCAGTGTGACAAGATCTACTTTTCTTCAGCGAGACTGCCAGGAA
TTTGAGTTCTTGAGAACACCATTGTGTCGGCATTGCCGCATCTGCAAGGGCAGTGGAGGGTGGAGAGCGGGGTG
CTACAGCAGCCTGGACCTCCTCCTCAAGGCCAGCTGCTGCTCACGGCCGACGATGGCTTCCCCTCAAC
GTGCTGAGGATGCTTACGCTGAGCCCCAGGCCAGGACTGGCGTACACCCTTTCTATGGGTCTCACT
TCCCAGTGGCACAGGGAACTACAGAAGGCTGCGCTGTTGCTTACAATGAAGGATGTGAGAGACTTC
AGCGGCCTCTACAGGAGGTGACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTCCCCACACCCGG
CCTGGAGCGTGCATCACCAACAGTGCCGGGAAAGGAAGATCAACTCATCCCTGCAAGCTCCAGACCGCGTGC
AACTTCTCACAGGACCACTTCTGATGACGGGAGGTCCGAAGCCGATGCTGCTGTCAGCCAGGGCTCG
TACAGCGCGTGGCTGACCGCGTCCCTGGCTGACCCACACTACGATGCTCTTCTGGGACTGGTGC
GGCCGGTCCACAAGGAGGTGAGCGTGGGCCCCGGTGCACATCATTGAGGAGCTGCAAGATCTCTCATGGGA
CAGCCCGTGCAGAATCTGCTCTGGACACCCACAGGGGGCTGCTGATGCGGCTCACACTCGGGTAGTCCAG
GTGCCCATGGCCAAGTGCAGCTGTACCGGAGCTGCTGGGACTGCCCCTCTCGGCCCCGACCCCTACTGTCTGG
AGCGGCTCCAGCTGCAAGCACGTGAGCTTGCAGCGCTTCTGGTTGTCAGCTGGGACTGCCCCTCTCGG
GGAGCCAGCGCAAGGACCTTGAGCGTCTCGGCTTGTGCTCCCCTCTTGTACCAACAGGGAGAAGCCA
TGTGAGCAAGTCCAGCTGCCAACACAGTGAACACTTGGCTGCCGCTCCTCCAAACTGGCGACCCGA
CTCTGGCTACGCAACGGGCCCCGTCATGCCCTCGGCCACGTGCTACCAACTGGGACCTGCTGCT
GTGGGACCCACAGCTGGGGAGTTCCAGTGTGGCTACTAGAGGGAGGCTTCCAGCAGTGGTAGCCAGCTAC
TGCCCAGAGGTGGTGGAGGACGGGGTGGCAGACAAAACAGATGAGGGTGGCAGTGTACCGTCTATTATAGCACA
TCGCGTGTAGTGACCGAGCTGGTGGCAAGGCCAGCTGGGTGCAAGACAGGTCTACTGGAAGGAGTTCTGGT
ATGTGACGCTTTGCTGGCGTGTGCTCCCAGTTTATTCTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCGTGGTGTGCCCTGAGACCCGC
CCACTCAACGGCTAGGGCCCCCTAGCACCCCGCTCGATCACCAGGGTACAGTCCCTGTCAGACAGCCCCCG
GGGGCCCGAGTCTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTGTGGAGGTATCCCAGTG
TGCCCCCGGCCCGGGTCCGCTTGGCTCGAGATCCGTGACTGTGGTTGAGAGCTGACTCCAGAGGACGC
TGCCCTGGCTCAGGGCTGTGAATGCTGGAGAGGTCAACTGGACCTCCCGCTCTGCTCTCGGAAAC
ACGACCGTGGTGCCTGGCCCTGGAGCCTGGAGGCCAGCTGCCCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCAACCGACACCCAAACAGCGTGGCCCAGAGGTCTGCCAAATATGGGGCCTGCCAGTGGTGGAA
CAGTGCTCTTATGTAACACTGAGCCCTTGTAAAAAAACAAATTCCAATGTGAAACTAGAATGAGAGGGAGAG
ATAGCATGGCATGAGCACACAGGCTGCTCCAGTCACTGGCTCCAGGGTGTGGGATGATCCAAAGTGG
TTGCTGAGACAGAGTTGAAACCTCAGCAACTGGCTCTTCCACATTATCCGCTGCCACCGGCTGC
CCTGCTCACTGAGATTCAAGGACCAGCTGGCTGCGTGCCTGCCAGTGGCACTGCCAGGGCTCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACCACCTCAGGGACCAGAGGGTAGGTTGGCACTGCCAGTGGCTGCCAGGGCTCAGCCGAGGAGA
GGACCCAACCTGGACCTTCCAGGCTGTATCAGGCTGTGGGACACAGGAGGACAGCCGAGCTCAGGAGAGA
TTTGTGACAATGTACGCCCTTCCCTCAGAATTCAAGGAGAGACTGTCGCCCTGCCACCGGCTG
GAACCCGTGTGCCCTTCCACCATATCCACCCCTGCTCCATTTGAACTCAAACACGAGGAACACTGCA
CTGGTCTCTCCCCAGTCCCCAGTTCAACCTCCACCTCCACCTCCACTCTAAGGGATATCAACACTGCC
AGCACAGGGGCCCTGAATTATGTGGTTTATACTTTTAATAAGATGCACTTATGTCACTTTTAATAAAA
GTCTGAAGAATTACTGTTAAAAAAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLQLPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLVVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYGTVSSFQGNDPAISRSQLRPTKTESSLNWLDQPAFVASAYIPE
SLGSLQGDDDKIYFFFSETQEFFECTIVSRIARIICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFNFNVLQDVFTLSPSPQDWRTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTWTVPPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFILMDGQVR
SRMLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNIATR
LWLNGAPVNASASCHVLPDGLLLVTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSPVIIISTSRVsapAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHNSM
KVFLQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCCGGCGGCCGGCTACGAAGAGGACGGGGACAGGCCGCGTGCAGACCGA
 GCCCAGCCAGCCGGAGGACGCCGGCAGGGCGGACGGGAGCCCAGCTCGTCTGCCGCCGCGTCGCGCGTGC
 TGCGGGCCCCGCCGTCCCCGCCGAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCGCCCTAGCGCGC
 CGGGCATGGTCCCCCTTAAAGGCAGGCCGAGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CCTGCGGCGGCTCGGGGCCGATGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CGCGCTAGGGCGGGCTGGCTCCGTGGCGGGGAGGGCGGGCTGAGGGCGCGGGAGGCTGCCGCCGGCG
 GGCAGGCCGGCGGCCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 ATGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC
 TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGGGCTCGTCTGCCGCCGGGGCTCCAGCTGAAGCGAGCG
 GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGCTCCGGCAGGCGGGCTTCCAGGCCGGGGGCCGCC
 GCGATGCCGCCGGGGCGAGCTCTGCCGCCGGCTGGACCAGATGCCGCCGCCGCCACAGGAACATTCTCT
 TCGTGGAGTCATGACGCCAGAAATACCTGCAGACTCGGGCGTGGCGCCCTACAGAACATGGTCCAAGACAA
 TTCCCTGGGAAAGTCAGTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
 GTGTGGACGACTCTACCCGCCAGAAAGAAGTCCTTCATGATGCTCAAGTACATGCACGACCAACTTGGACA
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCTCTTCTTGGCAGACAGGCCTGGCACCCAGGAAGAAATGGAAAATGCCCTGG
 AGCCTGGTGAGAACCTCTGCATGGGGGGCTGGCGTGTACATGAGCCGGAGGTGCTCGGAGAATGGTCCGC
 ACATTGCCAAGTGTCTCCGGAGATGTACACCACCATGAGGACGTGGAGGTGGAGGTTGTCGGAGGTTG
 CAGGGGTGCAGTGTCTGGCTTATGAGATGCCAGCTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
 ACATTAGAGATCTCCATAACAGTAAAATCACCAAGCTATCACATTACACCCAAACAAAACCCACCCCTACCA
 ACAGGCTCCACAGCTACATGTCAGGCCAAGATATCCGAGCTCCGCCATCGCACAATACAGCTGCACCGCGAAA
 TTGTCTGATGAGCAAAATACGCAACACAGAAATTCTATAAGAGGACCTCCAGCTGGAAATCCCTCCCTCCTCA
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGAGTTCTGACTGGAAAATACTTGTATTCCGAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAAGCCTGGACGACATTGTATGCAGTCA
 TGGAGATGATCAATGCCAACGCCAAGACCAAGAGGGCCATCTGACTCAAAGAGATCCAGTACGGCTACGCC
 GGGTGAACCCCATGATGGGCTGAGTACATCTGGACCTGCTCTGTACAAAAAAGCACAAAGGGAAAGAAAA
 TGACGGTCCCTGTGAGGAGGCAGCGTATTACAGCAGACTTCTGAGCAAATCCAGTTGTGGAGCATGGAGC
 TGGATGACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTCTCTCAAACCTCCCTGAAGA
 AGCTCGTCCCTTCAGCTCCCTGGCTCGAAGAGTGTGAGCACAAGAACCCAAAGATAAAAGATAAACATACTGA
 TTCCCTTGTCTGGCGTTTCGACATGTTGTGAGATTATGGAAACTTGTGAGAAGACGTGTCTATCCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTCAATTCTGACTCCAACCCCTGACAAGGCCAACAAAGTGAACGTGATGA
 GAGATTACCGCATTAAAGTACCCCTAAAGCCGACATGCAGATTTCGCTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCCTGGAAGTAGGATCCTCCAGTTAACATGAATCTTGCTCTCTCGCAGCTCGACCTCGTGTACTA
 CAGAATTCCCTCAGCGATGCGAGCAAATACAGTTGGCCAACAAATATATTTCCAATCATCTCAGCCAGT
 ATGACCCAAAGATTGTTATAGTGGAAAGTCCAGTGACAACCATTGCTCTTACTCAGAAAATGGCTTCT
 GGAGAAAATGGTTGGCATCACGTGATTTATAAGGGAGATCTGTCCAGTGGGTGGCTTGATGTTCCA
 TCCAAGGGCTGGGGCTGGAGGATGTGCACCTTTCAACAAGTTGTCCAGGAGGTGAAAGACTTAGGAGCC
 AGGAAGTAGGAGTAGCCACGCCATCTGTCTTTGTGATCCAAATCTGACCCAAACAGTACAAATGT
 GCTTGGGGCTCAAAGCATGCCATCTGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGAGCAGCTAATGTCCAGCTTGTCTGGAAAAGACGTTT
 TAATTATCTAATTATTTCAAAAATTTTGATGAGTCAAGTGTGAGTTTGAGTCCAGTGTGAGTCCGTATA
 AAGTGGTTTCTTACATAGGACTCTTAAAGTGTGAGCTCTGAGAACAGGAGTGTGAAACAAAATTT
 CACATCTCTGCTGAACATTATGTGAGCACCTGCTTAACCTTAACTTGTGAGTCCAGTGTGAGTCAAGT
 TTTAAAAAAATGTTTCTTGTGAGACCTTGTGCTCCAGTCTATGGCAGAAAACGTGAAACATTCTGCAAAGT
 TATTGTAACAAAACACTGTAACCTGGTAATGTTCTGTTGATGTTAACATTCCACAGATTCTACCTTTGT
 GTTTGTTTTTTTACAATTGTTAAAGCCATTGATGTTCCAGTTGTGAGATAAGGAAAATGTGATAATA
 GCTGTTCATCATTGCTTCAGGAGAGCTTCCAGAGTTGATCATTCTCTCATGGTACTCTGCTCAGCATGG
 CACGTAGTTTTGTTGTTGTTGTTGTTGTTGAGACGGAGTCTCACTGTGTTACCCAGGCTGGAAATG
 CAGTGGCGCAATCTGGCTCACTTAAACCTCCACTTCCCTGGCTCAAGCAATTCCCTGCCCTCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATTAGTAGAGACGGGGTTCACCAT
 GCAAGCCCAGCTGGCCACGTAGGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTG
 TGGTAGTTCACTGGCTAAATAGACCTGGCATTAAATTCAAGAAGGATTGGCATTTCCTCTGACCCCT
 CTCTTAAAGGGTAAATATTAAATGTTAGAATGACAAAGATGAATTATTACAATAATCTGATGACACAGACT
 GAAACATACACACATACACCCCTAAACAAACGTTGGGAAAATGTATTGGTTTGTGAAACACCTTAA
 TGTGTTATGTGGGTGGAGATGGTTTCATTCTTCAATTACTGTTGTTTATCCTTGATCTGAAACACCTTAA
 TTTATTAAATATCTGTTGTCAGAGCTGCCATTCTGAGTACCTGTTAGTTAGTATTATGTGATCGG
 GAGTGTGTTAGTCTGTTTATTGCACTAAACGATCTCCAAAGATTCCCTTGGAAACGCTTTCCCCTCC

FIGURE 143B

TTAATTTTATATCCTTACTGTTTACTAAATATTAAGTGTCTTGACAATTGGTGCTCATGTGTTTGGG
GACAAAAGTGAATGAATCTGCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTCAATTGGAGGGCTGCGTATTGAAATAG
CCTGATGCTCATTGGAAAAATAAACCGAGTGAACAATATTTCTATTGACTTTCGAACCACTTGTCTCATT
ATTCCCTGTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
 ><subunit 1 of 1, 802 aa, 1 stop
 ><MW: 91812, pI: 9.52, NX(S/T): 3
 MAARGRRAWSVLLGLVLGFVLASRLVLPRASELKAGP RRRASPEGCRSGQAAASQAGGAR
 GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGVQFFSSEG
 SDTSVPPIPVPVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRA DDDVYIKGDRLENFLR
 SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
 THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
 YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKE DLQLGIPPSFMRFQPRQREE
 ILEWEFLTGTGKLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
 GYRRVNP MYGA EYILD LLLYKKHKGK MTPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
 INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVR FMGNFEKTC
 LI PNQNVKL VVLLFNSDSNP DKAKQVELMRDYRIKYPKADM QILPVSGEFSRALALEVGSSQ
 FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
 QKTGFWRNYGFGITCIYKGDLRVGGFDVSIQGWGLEVDLFNKVVQAGLKTFRSQEVGVVH
 VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCATGAAGCCTTAGTCCTCTAGTTGCGCTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAAATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGGCCAGAGCCAGAGCCGGAGCCAGCTGAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCA
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTTAGATATTAATTCAAGTGCAACAGGCACCTTCTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAATATGTGAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTATTAAACAATAATATAAAAATTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAAC TGCA TTTTCACAGGAGAAATAATCATATTGCAAAAGTTGTAT
 AAAAATATTCTATTGAGTTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTTAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSVILHAAE PYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSQVQQALLSDTSNPA
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVV
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCAAATCATCCATCCACCCCTGCTGTCATCTGTTTATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTGGTCTCAGTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTACAGAGATGGGAAGACTGGAACTTAAGCAGATGCCACA
 GTATCGAGGGAGAAGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTCAAGTCCCAGATTAC
 GATGAGGAGGCACCTGGAGCTGCAGGACTGGCTCACTCCTCTCATTCCAT
 CGTGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTAGTCCAGGAAAATGCTGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTCCAGCCCTCACCTGGGCCTGGCTTCTATTAACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAGGGAAAATCCA
 GGCAGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCCTTGATCTGAAA
 ACTGTAACCCATAGAAAGCTCCCCCAGGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAAATGTG
 ACTTTGTCTCCAAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC
 ATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCTACAGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTCTCAATACAAATGACCAGTCCCTATTATACC
 CTGCTGACATGTCAGTTGAAGGTTGAGACCCATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGACTCCCATATTCATATGTCAGTGTGTCCTGGGAT**TGA**AGACAGAGAACCCCTG
 CTTAAAGGGCCCCACACCAAGACCCAGACACAGCCAAGGGAGAGTGCCTCCGACAGGTGGC
 CCCAGCTCCTCTCGGAGCCTGCGCACAGAGACTCACGCCCTACTCTCTTAGGGAGC
 TGAGGTTCTCTGCCCTGAGCCCTGCAGCAGCGCAGTCACAGCTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGACGGAATAGACTCA
 CATTAGGTTAGTTGTGAAAATCCATCAGCTAAGCGATCTGAACAAAGTCACAACCTCC
 CAGGCTCCTCATTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTGCAAGGTTGAGGGCACAGTGTGCTAATGATGTGTTTA
 TATTATACATTCCCACCATAAACTCTGTTGCTTATTCCACATTAAATTACTTTCTCTA
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTAAACAAATAAACTAAACAAATATTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAATCAACCAGTGTAAATT
 CAGCACATTAAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFKVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQOPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVASQGFQAGRHYWEVDVGQNVGWWVGCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTGTTGGGAACCCCTGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTCATTATGTGAGATATAATCAAAGAACCTACAA
 TTACTATAGCACATTGTCATTACAAC TGACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
 TCTCCATTAAGGGAAAGAATTGTCAGTCTCAGGTATCAAGTTCAACAGAACGATGG
 AGTGTGGCTCATATGCTGTTGATTGAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGAGGACCCCCTAAAGTA
 GATCCTCACTCAGTAAAATTAAAAAAATCAACAAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTCGGAACACGAAGAAGTAAAACCTAGGTCAAGACTCAGGATCGTTGGTGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTGTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCCGCCAGATGGACTGCTCCTTGGAGTAACAATAAACCTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTCCTACACAAATGCAGTACATAGAGTTGCTCCCTGA
 TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAA
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTGGAGGACACTGGTAGTTCAAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTAACTAGAGTTACGGCCTTGCAGGACTGGATTACTTCAAAACTGGTATC**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTTTGGGTGTGGAGGCCATT
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCTAGGTTCTCTAGAAGTTGTCAGAATTGAC
 TTGTTGACATAAATTGTAATGCATATATAACATTGAAAGCACTCCTTCTTCAGTCCCTC
 AGCTCCTCTCATTCAGCAAATATCCATTTCAGGTGAGAACAAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTGAAAGGTCAAGCAAAGACAGCAGAACATACCAATC
 ACTTCATCATTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAACGCAAGATATA
 TCCTTATTTCTTCAACAAACTACTATGATAAATGTGAAGAAGATTCTGTTTTGTG
 ACCTATAATAATTACAAACTTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAAATAAAATATAACACCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPLREEFVKSQVIKFSSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKGRLRIIVHEKYKHPHDYDISLAELSSPVYTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

TO THE LEFT

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATAAACCTGACAGCA
 CAGCCTGAGATCTGGGGATCCCTCAGCCTAACACCCCACAGACGTAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTCTGTGGCTCCTGGC
 CGTGACCTTCTGGTTCCCAGAGCTCAGCCCTGGCCCCCTCAAGACTTGAAGAAGAGGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCTTGCCGGCTGTCCCCTGCGACTACGACCACGTG
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCACATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTTCTCCCCGGCTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAACCTGAAGGGGCTGAAGCCAGGGGCATTATGTCGTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGCAAGCCCGTGCCTGCCAGGCTGGAGGGAGAGGGCCTCGAGGGGCCGACATC
 CCTGCCTTCGGGCCTTGCAGCCGCCCTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
 GGCGTCGGGTGGCACGCCCTGGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCAGTCGCTGGGCTGCCCGCCGAGCCGCCGAGCCCGCAGGGCGCTC**TGA**
 AAGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGGCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG
 GCTCCAGGGCCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTTA
 AGCGGCCAGATAATAATGTAACCTTGCGGTTAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCGPLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAAGVGVTALALLSCAALVWHFCLDRWGCPRRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAAGAACGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCC
 CTGCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCAGGCAGGGCGTGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTAAAGGATGGGC
 TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACAGCAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCCGTGGTCATCCGGTATGATTGCTGTTGCTGTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTAACGGTAAAAGAAATCTGTTGCTCTGCATGGTACT
 TTGGAAGTTGCTGTCAATTCTGTGAGAACTGGCTGTGGCTTGGACATATGAACAG
 GAACTATGGTCCAGTACAATGGTCAAGATATGGTCACTTGAAGGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTCAGAGAGATTTAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTATCAAGAGGGTGTGGGAAGAAAATGTATTCTTTGAGAGGAACCAAACACTGC
 AGGTGCTGAGGTTCTGGGAATCTCATTGGGTGACACAAATCCTGCCATGATTCTCAC
 ATTACTCTGCTCTGGCTCTGTATTATGATAGAACAGGGAGCCTGGACAGACAAATGATGTC
 CTTGAAGAATGACAACACTCAGCACCTGTATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAATACACACTTGGAGATGGAG
GAGTTAAAAAAGAAATGTCACAGAACACACAAACTTGTATTGGACTGTGAATT
 TTTGAGTACATACTATGTTGAGAAATATGAGAAATAAAATGTTGCCATAAAATAACA
 CCTAACGATATACTATTCTATGCTTAAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTACACCCACTGTGTC
 CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTATTACTCAGCGATCTTCTGATGCTAAATAATTATATCAGAAAACCTTC
 AATATTGGTACTACCTAAATGTGATTTGCTGGTTACTAAAATATCTTACCACTTAAA
 GAGCAAGCTAACACATTGTCTAACGCTGATCAGGGATTTGTATATAAGTCGTGTTAAA
 TCTGTATAATTCACTGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGCTGTATAGCATCATTATTTAGCCTTCTGTTAATAAAAGCTTACTATTCTGT
 CCTGGCTTATATTACACATATAACTGTTATTAATTAACCTAACACTAATTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAAGAATGTAGTCTGGCTTTAGGAAGTATTAATAA
 GAAAATTGACACATAACTTAGTTGATTCAAGAAAGGACTTGTATGCTGTTCTCCAAATG
 AAGACTCTTTGACACTAACACTTTAAAAGCTTATCTTGCTCTCCAAACAAAGAA
 GCAATAGTCTCAAAGTCATATAAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTAAATTGTTACAAGAGTATAGTATATTGTT
 GAAATGGAAAAGTCATTTACTGTATTTGTGTTATTCAGAATATGGAA
 AGAAAATTAAATGTGTCAATAATATTTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGCCTCCAGCCAGTGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGAGGCCCTCCTGCTGCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAG**CATGTT**ACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCAGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTTCTGCCTGTTGACAACATTACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGCATCGGAACACTAACGTGGCCCTGTC
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTTGCCTGTGGAAAGAGCCTGAAGACCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATTGGACCCCCACTGGTCCTCACGGCAGCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
 AGCTTCCCACCCATGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACTCACTTCTCAGGCACAGTCAGGC
 CCATCTGTCGCCCTTGTGAGGAGCTCACTCCAGCCACCCCCACTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTCAATGCAGACGATGCGTACCAAGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGCATCGTAGCTGGGCTATGGCTGCC
 GGGCCCGAGCACCCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTGCAGTGCTGGAGCCGCTCCTCCTG
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGCCCTAACCTGTAAAGAGACCC
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAACCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCCGCTTCAACCCATCCCCAAGCCTA
 CTAGAGCAAGAACCAAGTGTAAATATAAAATGCACTGCCACTGTGGTATGACTACCGTT
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAAETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTQCQGDSGGPLMYQSDQWHVVGIVSWGYZGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
 AGCTCCCTGGTACAGTCTGTGGCTGAGC**ATGGCCCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCGGGCC**
 TTTCCCTTCCA**ACTGCTTCAGCTGCTGCCGACGACGCCGGGGAGGCCAGGGCCATGCCA**
 GGGTCAGATACTATGCAGGGATGAACGTAGGGCACTTAGCTCTTCCACCAGAAGGGCTCCAGGATTTGACA
 CTCTGCTCCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAACGCACTTCTGGCCTGGATATCCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCCAGCAGTGACAGAAAAAGAGTGAATGTGCCCTTA
 AGAAGAACAGCAATGAGACACAGTGTTCACCTCATCCGTGCTCTGGTTCTTACAATGTCACCCATCTACAC
 CCTGCACCTTCGCCTCAGCCCTGCTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCATCTCGG
 AGGACAAGGTATGGAGGGAAAAGCCAAAGCCCTTGACCCGCTCACAGCATACGGCTGTTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC
 CTGTCCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCCTTGTGGCAGCCATCCCTCGACCC
 AGGTCGCTACTTCTTCAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGCTCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAACATGACGTGGCGGGAAAAGCTGCTGCGAGAACAGTGGACCACCTCCTGAAGGCCAGC
 TGCTCTGCAACCCAGCCGGGCAGCTGCCCTCAACGTCACTGCCACGCCAGCGGTCTGCTCCCGCCATTCTCCA
 CAGCTCCCCACATCTACGCAGTCTCACCTCCCAGGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCCT
 TCTCTCTTGGACATTGAACGTGTTAAGGGAAATAACAAAGAGTTGAACAAAGAAACTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGCGTGGAGTATA
 CACGGCTGCAGTGGAGACAGCCAGGGCTTGATGGCACAGCCATCTGTCACTGACCTGGAAACCACACAG
 GGTGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGGAAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTGAGGCTCAGGAGGTGTCTGGA
 GGGTCCCCGAGCCA**ACTGTAGTGTCTATGAGAGCTGTTGACTGTGTCCTGGCCGGGACCCCCACTGTG**
 GGGACCCCTGAGTCCGAACCTGTTGCTCTGTGCCCCAACCTGAACCTGGAAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCTGAGCAGGAGCCTCGGCCTCAGAGCCGCCAAATCATTA
 AAGAACGTCTGGCTGCCCCACTCCATCCTGGAGCTCCCTGCCCTGCCCCACCTGTCAGCTGGCTCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAACGCTCTTCACTGTCATAACATGGCTCCCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGTCTCTACAGTGCTGGCAACTGAGAACGGTTTACCTGTCATGTCAGCTGGCT
 ACAGCCAGGACCAGCCCTGGATCCTGAACGGCATGCCCTGGCAGGCTCCAGGAGCATGTGAAGGTCCCCTGA
 CCAGGGTCACTGGTGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCACTTGTCACTGTCAGCTGCTCT
 TTGCCTTAGTGCTTCAGGAGCCCTCATCATCCTCGTGGCTCCCTTGAGAGCAGACTCCGGCTGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAACGGCCCTGTTAAGCAGAGAGCAACACCTCCAGTCTCCAAGG
 AATGCAGGACCTCTGCCAGTGATGGACGCTGACAACAACTGCCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA
 CAGGCCGGGCTGCCGTGAGGACGCCAGTGGCTGGGAGGGATCCCTAGTTCTGCCATTGAGAGCAGCAGGGT
 CAGCACAAAAGACCACTTCTCCCTGAGAGGAGCTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGT
 ATGCACAGCAGTCTGCCCTCCCTATGGACTCCCTACCAAGCAGCATGAGCTCTCAACAGGGTGGGGCTAC
 CCCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGAGCTGCTACTCTGCATCACTGATGACACT
 CAGAAACACAGTGTTCAGAGAACCTAAACCTGCCTGTCCAGGACCCATGGTAATGAACACCAAACATC
 TAAACAACTCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAGCTGCCCTGGACACCAACACTCCCT
 TCTCCCAAGGGTCACTGGGATCTGCTCCCTCTGCTCCCTTACCAAGTGTGCACCCGCTGACTCCCAGGAAGTC
 TTTCCCTGAAGTCTGACCACTTCTTCTGCTCAGTTGGGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG
 CAGGGGTAATCTGAGCCTTCTCACTCCTTACCTAGCTGACCCCTCACCTCTCCCCCTCCCTTTCTTGT
 TTTGGGATTCAAGAAA**ACTGCTTGTCAAGAGACTGTTATTTTATTAAAAATATAAGGCTAAAAAA**

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
 ><subunit 1 of 1, 761 aa, 1 stop
 ><MW: 83574, pI: 6.78, NX(S/T): 4
 MALPALGLDPWSLLGLFLFQLLQLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
 DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSEAFKKKSNETQC
 FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
 VLVDGMLYSGMTMNNFLGSEPILEMRTLGSQPVLKTDNFLRWLHHASFVAAIPSTQVVYFFE
 ETASEFDFFERLHTSRVARVCKNDVGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
 PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
 NPRPGCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
 YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPPEPVRLNLQAPTQGAVFVGFSGGVWRVPRAN
 CSVYESCVDCVILARDPHCAWDPEPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
 QSRPQIIKEVLAAPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
 LYQCWATENGFSYPVISYWVDSQDQLALDPELAGIPREHVVKVPLTRVSGGAALAAQQSYWP
 HFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
 SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCGTAGAAG
TGAGC**ATG**GCTGGCAGCGAGTGCTCTTAGTGGCTCCTCTCCCTGGGGCTGCTC
 TCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCAGCTTAACCACAAAAGAG
 GTCCTTTATGCCAGATTAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTTCTTCTGGAAGAAACTTAGG
 TGGCAGAGGAAAATTGAAAATTATTAAATGTTCTAGAATACCTGGCCTGCAGTCAGTC
 ATTTTAAATAGAAAGGATATCATGGATCCTTAAAGAATGAGAACATTCGACATGGTATA
 GTTGAACACTTTGACTACTGTCCTTCTGATGCTGAGAAGCTGGGAAGCCATTGTC
 CATTCTTCCACTTCATCGGCTTTGGAATTGGGCTACCAATCCCCTGTCTTATGTC
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTCTGGGGCGAGTGAAGAATTCTG
 ATGTTCTTCTGAGTTCTGAGGAGCAACAGCACATGCACTGAGTCTACATTGACA
 GGAAACATTTCACAGAAGGCTCTAGGCCAGTTGTCATCTTCTACTGAAAGCAGAGTGT
 GGTCATTAACCTGACTTGCCTTGATTTGCTGACCTCTGCTTCCAAACACTGTTAT
 GTTGGAGGCTGATGGAAAACCTATTAAACAGTACCAAGACTTGGAGAACATTCATTG
 CAAGTTGGGACTCTGGTTTGACCTGGCTCCATGGGAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAACAATGCCTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGGCCAAGATGTCCACCTGGCTGAAATGTGAAAATTG
 CTGGCTTCCTCAGAGTGACCTCTGGCTCACCAAGCATCCGTCTGTTGTCACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGTGTCTATT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTACATCCTGCGCTCCACCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCC
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCACGTTTGTTGTCCTGCTGGG
 TCACTCTGGGACTCTATGGCTTGTTGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTGGCGGGCTGTTGG
 GCGATGTCACCATTCTAGGGAGCTCCACTAGTCTGGCAGCCCCATTCTAGTC
 TAGTTATCTCCTGTTCTGAGAACAGGAAAATGGCAAAATCATCCTTCCACTG
 TAATTGGCTACAAATTACATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTCCAGTC
 CTTGTCCTCCTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACT
 GACCACTGACCCCTCAGATTCCAGCCTTAAACATCCACCTCCTCTCATGCGCCTCTCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCAGACCTAGTCAGCCTCTCACTCCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTCTTCAGTTCTG
 TGTTCTCCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTT
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTGGTGCCCCACAGTGAGCT
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAAAATAAAAGTTACA
 CGCTTATCTCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPNTVYVGGLMEKPIKPVQPQDLENFIAKFGDGFVLTGSMVNTCQNP
EIFKEMNNNAFAHLPGQVIWKCQCQSHWPKDVLAAANVKIVDWLPQSDLLAHPSIRLFVTGGQ
NSIMEAIQHGVPVMVGIPLFQGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGTCTCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGCAGGGCGCTTCATCCCTCCTCTCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAACAGAGGGGCAGA
 AGACCGGGGCACTTGTGGTTGCAGAGCCCTCAGCC**ATG**TGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCACACAGTCCGGCTGCCCTTGGTTCTGGTGCCTCTGGCCTGGGGGCC
 GGGTGGGCCAGGAGGGTCAGAGCCGTCCTGCTGGAGGGGAGTGCCTGGTGTGTA
 GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCATGAGCCAGCAGGGAAACCCGGCAATGGC
 ACCAGTGGGCCATCTACTCGACCAGGTCTGGTGAACGAGGGCGTGGCTTGACCGGGC
 CTCTGGCTCCTCGTAGCCCTGTCCGGGGTGTCTACAGCTCCGGTCCATGTGGTGAAGG
 TGTACAACCGCAAACGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCATGAGCTCTGTGCTACTGCCCTTGA
 CCCTGGGGACCGAGTGTCTCTGCCCTGCGCTCGGGGAATCTACTGGTGGTGGAAATACT
 CAAGTTCTCTGGCTTCATCTTCCCTCTC**TGA**GGACCAAGTCTTCAAGCACAAGAAT
 CCAGCCCCTGACAACCTTCTTCTGCCCTCTTGCACCCAGAAAACAGCAGAGGAGGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTGATGGGACCCCTGTGCCAAACACCCAAAGTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCCAGGCCTTCCACCCACCCACCCAGTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCTGCCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCACACTTGGCATCCCAGATGGACTCTGGCCCTTACCTCCCCACCCAGCTCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCACAGGAGGCCAG
 ATGGACAAGCCTCAGCGTACCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCGTGGCTGGTGAAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATAAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTGAACCTTACTGCTCCCTCCACACTCTGACTGCTGCCTCCTCCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTTCTCCTGAT
 CTGTGCTGTCTTATTCTCCTCTAGGCTCCTATACCTGGATTCCATGATTCAATTCTT
 CAGACCCCTCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTTCTTATCCCGCTGCCCCATT
 GGCCAGCCTGGATGAATCTATCAATAAAACAACAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAATCAAACGTATACTAAAATTAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGPLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFAFPDVTRREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

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FIGURE 163

GCTGTTCTCTCGGCCACCACTGGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC
 CTCGACGCCGTCCCAGGGACCCCTGTGCTCTGCAGAAGCCCTGGCCCCGGGGCCGGGCAT
 GGGCAGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCGTGACTGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCCTACTCCGGGGCCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGCGCGAGGGGTCTGGGAGATGGGCACT
 GGATCCAGCATCCTCTCCGCCCTCCAGGACCTTCTCTGTCACCTGGCTCAATAGGTCAA
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCCTGTCCTCCTGTACTGG
 GAGTGGCCTGCAGTGCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG
 CTCTACTTCACTTGGCTGGTGTGACTGAAACACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAAACTGGGCTGTGTCAGCGCTACTTCGAGACTACTTCCATCCAGCTGGTA
 AGACACACAACCTGCTGACCACCAGGAACATATATCTTGGATACCACCCCCATGGTATCATG
 GGCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG
 CATAACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCTGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATAAGACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGTGCAGCTGAGTCTCTGAGCTCCATGCC
 TGGCAAGAACATGAGTCACCCCTGCGGAACCGCAAGGGCTTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTGGAGAGAAATGAAGTGTACAAGCAGGTGATCTC
 GAGGAGGGCTCTGGGCCGATGGTCCAGAAGAAGTTCCAGAAATACATTGGTTCGCCCC
 ATGCATCTCCATGGTCGAGGCCTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACGTGTTGTGGAGAGGCCATCACCATCCCCAAGCTGGAGCACCCACCCAG
 CAAGACATCGACCTGTACCAACACCATGTACATGGAGGCCCTGGTAAGCTCTCGACAAGCA
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTCTGAAATTGGAAGTGTCA
 TGGGTGTCTGTGGGTATTTAAAGAAATTATAACAATTGCTAAACCAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTЛИAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKKGGRRS
QWVRNWAWRWFРDYFPIQLVKTHNLLTRNYIFGYHРHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVЛREYLMSGGICPVSРDTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHГRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLHHTMYMEALVKLFDK
HKTKFGLPETEVLEVН
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGGGGATGGGGCCGGGGCGGCCGCGCCACTCGCTGAGGCCCGACGCAGGGCGGGCGGGCCA
 GGGCGAGGAGCGCGCGGCCAGAGCGGGCGCGAGGCACGCCGGGACGCCCGCGACGAGCAGTGGCG
 CGGGCTGCAGGCTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCCTGCTGACCTGTGCCTTGA
 CGGCTGTCCTCAGCGAGGGCGCTGCACCGCTCTGAGCAGCGCC**ATGG**GGCCTGCTGGCCTCCTGA
 AAGACCCA
 GTTCGTGCTGCACCTGCTGGTGGCTTGTCTCGTGGTGA
 GTGGTCTGGTCAACTCGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCGGTCA
 GAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCTCGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGTGGCTGCACGGAGTGTACACTGTTCACGGACCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACCGAGTCATCATCCTCAACCACA
 ACTTCGAGATCGACTCCTCTGTGGTGGACCATGTGTGA
 GCGCTTCGGAGTGTGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGACACCGTGGTCAAGGGCTGAG
 GCGCCTGCGGACTACCCGAGTACATGTGGTTCTCCTGACTCGCAGGGGACGCCCTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAACGGGCTTCTGCTCAAGTACCACTGCTGCCGCGACCAAGGG
 CTTCACCAACCGCAGTCAGTGCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
 CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCCACATGTGCGTGGAGGAGATTCTCT
 GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTAGTGGCTTCATAAAACTGTACCAAGGAGACGCGCTCCA
 GGAGATATATAATCAGAAGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
 CTTCTGTCCTGGGCCACCATTCTCCTGCTCTCCCTCTCAGTTGTCTGGCGTCTTGCCAGCGGATCACC
 TCTCCTGATCCTGACTTCTTGGGTTGTGGAGCAGCTTCCCTTGAGTTGCTCGCAGACTGATAGGAGAATCGCT
 TGAACCTGGGAGGTTGAGATTGCA**G**AGTGTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTAAAAAAAAAAACAAAAACCCCCAGAAATTCTGGAGTTGAACGTGAGTTACTGACATGAAAA
 ATTCACTAGAGGCTAACAGCAGATTGAGCAGGCCAGAAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT
 TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCCAGAACGGAGAGAACGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCTAT
 ATCAAAGTCTAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTG
 ATCAGATTAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
 AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTCTTGCTTCAGGGACAGTTTCA
 ATTTAATCCCTAATAACAATTAGTCAGCTTCCCTGACCTGTAGGAAGGCCGTCTTAGGCCGGCACAGTGGC
 TTACACCTGTAATCCCAGCACTTGGGAGGCCAGACGGGTGGATCATTGGGTCAGGCTGATCTCAAACCT
 GAGTTCAAGGTGATCTGCCGCCTCAGCCTCCAAAGTACTGGGATTACAGGGTGAGCCACTGCGCTGGCGGA
 ATTTCTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCGTGATCCAAGTAGCTTGGATTGTA
 AACATGCACCAACCATGCCTGGCTAATTTGTATTTTAGAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCTCAGCCTCCAAAGTACTGGGATTACAGGGTGAGCCACTGCGCTGGCGGA
 GCATCTTGTGATGTGCTTATTGCCATTGTATATCTCTATCTTCTTGAGGAAATGTCGTTCAAGTCCTTG
 CCTTTAAATTTTATTATTATTATTATTGAGACAGGGCTTGTGTCAGTGTGATCTCCACCTCAGCCTCCCT
 AGTGGCACAGTCTGGCTCACTGCAGCCTCGACCTCTGGCGTGCAGTGTGATCTCCACCTCAGCCTCCCT
 AGCTGTATTTGTATTTGTAGCTGTAGTTGTATTTGTGGAGACAGCATTCAACCATG
 TGCCAGGCTGGCTTGAACCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACACACACACACACAC
 GAGGGGCCGGGTGTGGCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCGTCT

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

2247007

GATATTCTTATTTAAGAACCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATTTGTGTGTTTCTTTGCTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTGGTAGGAAAGGGGCTCAGTTGTCTGGGGTTGGCAGGCAGGCCG
 GCTTACGCCTGATAACGCCCTGGGTTAGAAGGGAAGGAAAGATAAAACTTTATACAAATGGG
 GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTCTT
 TTCTCTAACCTGGCATACCCCTGCTAAAGCCTCTCAGGGCTCTCTGTTCTAGGATCAA
 AGTATTAGAGCTACAAGAGCCCTCATGGCTGGCCCTGCCCTGGCCAGCTTCAATTGT
 ACATGTGGTGTCTTGTGTTCTGTAATGTGGTATGCCATGGGTCTTGACAAAGCCT
 TTCCTCTTGGCTGGACACTGTTCCCTGCCCTGGGACTACTCTTCCTACTTAATATGTAGTC
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCTGGCCTGACAGAATCTCAT
 CTTGTTAATGCTCTCATAGACCCTTGTGTTCCCTTGAGCACTGCCACTCAGTTGTA
 TCTTTATGTGCGTTGTGGTTGTATGGGTGTGCTGTTCCCCAGAATGCCAGCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGCCTACATGTGGTGGTGCT
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTACCA
 GATGGTAGGGCCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGA
 TGCAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGTGGC
 TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCAACATGGTGGAACCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWRR
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTCAAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTCTGTAACTAGCCTTACCTTCAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTCAGGTAGCTGAGCCTTTGGTA
 GCTGCGGCTTCAAGGTGGCCTTGCCCTGGCGTAGAAGGGATTGACAAGCCGAAGATTT
 CATAGGCATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTTCATGTCCGCACATCACCTGATCCATGGCTAAATCTGAACTCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGACATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGGAACTTGTGCCAAATTATGGTCAGAAAAGATGGAGGTGTTGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCGATCCACGTACAGCTGCTG
 AAGGGCAACTGCAGGCCATGCTCTCATGCCAGGCAGCAGCCAAATCTGCATCACCAG
 CCAGGGCAGCGTCTGGAAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCCTC
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCCAGGAGGTCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGCCCTATAACCCAGGAGACTTGATTTGAATTGAAACCCCAA
 TCCAAACCTAAGAACCGAGGTGCATTAAGAACAGTTATTGCCGGGTGTTGGCTGTAATG
 CCAACATTTGGGAGGCCAGGCGAGGCGGGTAGATCACCTGAGGTCAAGACAGCAGCCTG
 GCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGGCCCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCC
 CCGCCGCCTCCTGCCCGGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCGCCGCGCT
 GCCCCTGGGCTCAGCCGCACTGGCGCCGCCTCGCCACTGGCCTCTCCTGGGGAGGC
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTCCCCCGAGGA
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC
 TGGCGGGCTCATCCAGCCAAGAACGGCGCTGGACCTGGCACCTTCACGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCCGGAGCTGGACGGCCCCCTGGAGGGCAGGCCGAGGCCGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCTTGGAGACCCCTGGACGAGCTGCTGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCCTGTGGCGCGGGAAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGCGAAACCTAAACGAACGCATCCGGCG
 GACGTCAAGGTCTACATCAGCCTCTGCCCTGGCGATGGACTCACCTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGAAACCCAGGAATTGAC
 CCTGAGTTTAAATTGAAAATAAGTGGGGCTGGGACACAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCAGCCGCTACCGCCGCTGCAGCCGCTTCCGCCGCTGGGCCTCTGCCGTCA
GCATGCCACACGCCTTCAAGCCCCGGGACTTGGTGTGCTAAGATGAAGGGCTACCCTCAC
 TGGCCTGCCAGGATCGACGACATCGGGATGGGCCGTGAAGCCCCACCAACAAGTACCC
 CATCTTTCTTGGCACACACGAAACAGCCTCTGGGACCCAAGGACCTGTTCCCCTACG
 ACAAAATGTAAAGACAAGTACGGGAAGCCAACAAGAGGAAAGGCTCAATGAAGGGCTGTGG
 GAGATCCAGAACACCCCCACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCGAGGCCAACCCGCCAGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCCGTACAGCGTAACGCCACAGCTGCCAGCAGAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAAACAGTGGCCTGAAGAGGAAGACGCCCTGCGCTAAAGATGTC
 GGTCTCGAAACGAGGCCAAAGGCCCTCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGCCCTCTGGGGGACGGAAAAAAAAGAA
 GGCGCCGTACGCCCTCGACTCCGACTCCAAGGCCATTGGACGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGTCGGCTCCTCCTCCTCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAACGCTCCGAGGGCAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCGCGAGG
 GCGGAAACCGAACGCTGAACGCCCTCCGTCCAGCTCAGCAGTGACAGCAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAAGCGCGGGACGAGGCGCGAGGCGCAGCTGGAGGCCGG
 CGCGGGCAGAGCAGGAGGAGGAGCTGCGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGCGAGCGGGCGACCGCGGGAGGCTGAGCGGGCAGCGCGCAGCAGCGGG
 ACGAGCTCAGGGAGGACGATGAGCCGTCAAGAACGGGGACGCAAGGGCGGGGGGGGT
 CCCCCGTCTCCTCTGACTCCGAGCCGAGGCCAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAACCGCAGTCCTCAAGCACAGAGGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
 TGCGGCCCGAGGAGAACACAAGCCAAGCCGTGAAGGTGGAGCGGACCCGAAGCGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAACAGAACAGGCCCTCCGTGGAGGGAGAAGCT
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGACAGGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGAACCCCTGCAGGTGACCTCTCAGATCCTCAGAAC
 ACAGACGTGGTGGCACCTTGAAGAACGATTGCCGTTACAAAGCGAACAGGACGTAATGGA
 GAAGGCAGCAGAACGACTATAACCCGGCTCAAGTCGCGGGTCTCGGCCAAAGATCGAGGCG
 TGCAGAAAAGTGAACAAGGCTGGGATGGAGAACGGAGAACGGCCAGGAGAACGCTGGCCGGGAG
 GAGCTGGCCGGGGAGGAGGCCAGGAGAACGGCGAGGACAAGCCCAGCACCGATCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGAACAGGAGCACG
 AGGAGGGCTGGACTCGGAGGAGGGCAAGGTGTGGCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGTCCCGACCTGGACAGGCCCTGGAGCGACGGCAGGAGCGCAGAGGGCACG
 GGGGAGCTCGGAGGCCCTGGACGAGGAGAGCT**TGA**GCCGCCAGCCAGGCCAGCCCCGC
 CCGAGCTCAGGCTGCCCTCTCCTCCCGCTCGCAGGAGAGCAGAGCAGAGAACACTGTGGG
 GAACGCTGTGCTGTTGTATTGTTCCCTGGGTTTTTCTGCCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAACGGTTTTAATGA

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNNKYPPIFFFGTHTAFLGPKDLPYD
KCKDKYGKPNKRKGFGNEGWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNGLKRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSEKTSQDFTEKKAAVRAPRRGPLGGRKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDVSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSDSDEV
DRISEWKRRDEARRRELEARRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSDSEPEAELEREAKKSAKKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNAL EELGT LQV TSQ I LQ KNT DV V AT LKKIR RYKANK DVM EKAAEV YTRLKS RL GP KIE AV
QKV NKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDLDRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGGTCTCCTGGATCTCACCTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATTTAAATTA
 ACACCATTGAAAGAGAACATTGTTCATC**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAACGCAAGA
 TTTTCACCTTTCTGCTTGATGATGCTAAGCATGACCAGTGTGTTCTTCCAGTCAGTGGCACTTGAAAGCA
 AAATAATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAAGAGGCAGGCTGCTTGGGAGCAGAACACAT
 CTTCTACTCAGTCTGGTGACTIONAACAAAATTAAAGAAGATTATGGCCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACTGGAGCATTCATCCAATATGTGGGTATATTGATCTGGAGTCTACAAGGA
 GGATATTATATTCAAACAGACACATAATTGGAGTCTGCAGACTGAAATGTCTTCGATCCTCAGCAGCC
 TTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
 CACTCGATCCCTGGGCCTACTCATGACCACACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTATTGGAACTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCCTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTGAGTTGGAAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCAGCCTGATAAACAAAGTGGACGACTTTCTAAGGCCAGACTGATTTGCTCAATTCTGGAAG
 TGATGGGCAGATACTTACTTGATGAGCTTCAAGATATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTACTACAACCAGCTCATCTCAAAGGCCTGCTGTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTGGGTGAGTATGATGGGAGAAT
 TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA
 TGATGTATCAGTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGGGATCATGTCATTGAGAAGATGGCCAGTACGA
 TGTAATGTTCTTGGAAAGACAGACATTGGAACTGTCCTCAAAGTGTGTCAGCATTCAAGGAAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTGTGAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
 GCAACAATTGTACATTGGTCCCAGATGGATTAGTAGTGTGACCTCTCTGACAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTGTTCTGCCAGAGACCCCTACTGCGCTGGGATGGAATGCGATCTCGATATGCTCCTAC
 TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAGGTTGGCATTGAATTAACTCAACCTTCTGGAATGTATACC
 TAAATCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGGATGAGCATCGAGAGGAGTTGAAAGCCGA
 TGAAAGAATCATCAAAACGGAAATATGGCTACTGATTGAGAAGGTTGCGAGAAGGATTCTGGGATGTATTACTG
 CAAAGCCCAGGAGCACACTTCATCCACACCAGTGAAGCTGACTTGAATGTCATTGAGAATGAACAGATGG
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
 CTACATCCAATCCTTAGCAGCCCAAACCTCAGCCTCGACCAGTACTGCCAACAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAAGGGGGCCCAAAGTGGAAAGCACATGCAAGGAAATGAGAAGAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGAATTCTTAC
 TATAAAAACATTGCCCTCTGTTGATATCCCTATAGTAAATTCAAAATGCTCCATGGAGTTTGCTAAGG
 CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAATTCAATTGAAACCAGTTT
 CCAAGAACAAATCTGCACAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGTAATGTTA
 TGTTTGAGTTTGGAAATTATTGTCATGTAATAGTTGAGCTAAGCAAGCCCCGAATTGATAGTGTATAAGGT
 GCTTTATTCCCTCGAATGTCCTTAAGCATGGAATTACCATGCAAGTTGTGCTATGTTCTTATGAAACAGATATAT
 CATTCCTATTGAGAACCCAGCTACCTTGTGGTAGGGAATAAGAGGTCAAGACACAAATTAAAGACAACCTCCATTATC
 AACAGGAACCTTCTCAGTGAGGCCATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTATTCTT
 TGGCCACTGGGTTAAATTAGTGTACTACAACATTGATTACTGAAGGCCACTAATTCCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAAGTTGGCTTAGTTGTTAGAGTATATACTAA
 GCTCTACAGGGACAGAACATGCTTAATAAATACTTAAAGATAGGGAAAATATTAAATAAAACAAAGGAAAACA
 TAATGATGTATAATGCACTCTGATGGGAAGGCATGAGATGGGATTGTTAGAAGACAGAACAGGAAAGAAC
 AAATTCTGGCTTGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAAATCACAAATTAAAGTGAAGAGTAATGTA
 TGGAGCTTTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCACTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAAACATAAATTCTCTGAGAACATAGGAAGAGTAGACATTATTATAACC
 AATGATATTCTCAGTATATATTCTCTTTAAAAAAATTATTCATACTCTGATATTATTCTTTACTGC
 CTTTATTCTCCTGTATATTGGATTGTTGATTATTGAGTGAATAGGAGAAAACAATATAACACACAGA
 GAATTAAAGAAAATGACATTCTGGGGAGTGGGGATATATTTGTTGAATAACAGAACGAGTGTAAAATTAAAC
 AACGGAAAGGGTTAAATTAAACTCTTGACATCTTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT
 GTAGTATTGTTTGTAAATTAAACAATAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLTYKDLLLNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAHDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLSTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTS DKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVI AEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKGACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPI TQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWIYIQRSGDEHREELKPDERI IKT EYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHHRD LDEL PRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAGGCCAGAGGTCACTGGAGCATGCCAACCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTATTTCCCCCACCCAC
CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTGTCCTGGAGTGGGAGCAGAAGGCCTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTAGCGCTTGACCAGCCAGCTGCCGTGACTACAAGATCCAGAACATGGGCATC
GGGTGAGGTGGGGGGCACAGGTGTCATGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGATCTGG
AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTGAGCTAGACGACATAGGTTCAAATTCTCTGTGCTTCCTAGTTCTGAGCCCCAGGT
AAGGGAGTGAACCTCTGGACTTCAATTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAAGATTAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAAGTCCCATAGTAAGTCATGCCAACAG
TATTCACCCACCCCTGTTCTGCCTCCCAACCCAGGTACTGCAACGACTGGAGCAGAGGGCGCAGCAGGCTT
CAGAGCGGGAGGCTCAAGCAGATAACAGAGGTACAGGAAGTGCAGAGAGGCATCCGCCGGCACAGGTGAGCC
AGGTGAAGGGGCTGCCGGCTGGCCCTGTCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGGCCAGCCA
TGACCCAGGGCAGGATGAGGTGGAGGAGCGGGCGCTCAGTGAGGCTCGGCTGCCAGAGGGACCTCTCTC
CAACGCTGAGGATGCTGAGCTTCTGACTTGTAGGAATGTGAGGAGACGGGAGAGCTCTTGAGGAGGCCAGG
CCCAGCCCTGGCACAGGGGCCCTCCCCCTGCCCTGCACACGTTGATTGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGTGAGTGGCTGGAGGTCAATAGAGGAGGGAGATGCTGACAATGGGCTGGAG
ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCATACTCAACTCCCCGACCTCTCCAGAGGAGCAGG
AAGACAGTGACAATCCCTGCGGGCAGAGCCCACAGCATTCTGGCACAGGCCCTGTACAGCTACCCGGACAGA
GTGCAGAGGAGCTGAGCTCCCTGAGGGGCACACTCATCCGTCGCTGCCCGGGCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGAGAATTGGGGCGCTGTTGGGTCTTCCCTCCCTGCTGGTGAAGAGCTGCTTGGGGCCC
CAGGGCACCTGAACCTCTGACCCCTGAAACAGATGCTGCCGCCCCCTCTCCCTCCAGCTTCCCCACCTGCAC
CTACCTCTGTTGGATGGGCCCCCTGCACCTGTCCTGCCCTGGGACAAAGCCCTGGACTTCCCTGGGCTCTGG
ACATGATGGCACCTGACTCAGGCCGATGCGTCCACCCACCTCCCCGCCGCTAAAGCCCCGGATCTGGGCCACC
CAGATCCCCTACCTTGAAGGCCAGGGAGCCTGACCCCCAGTGATGCTGCTCCATCTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAATGCCCTATTCCACCCCTCACCTCAAGGGT
GGAAACTGCCCCCTCCCATTTAGAGCTGGAACCCACTCCTTTTCCCATTGTTCTATCATCTTAGGACC
GGAACACTACCTCTCTCTGTCATGCCCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGGTTCTGGCCACCTCTTCCCCACCCCTGGCTCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGGTGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCCAGGATGCGAACAG
CTGTAATGGCTGAGCGGATTATTGACAATGAATAAGGGCACGAAGGCCAGGGCTGGGCTCTGGCTCTGGT
CTAAGAGGGCAGGGGCTACGGTCTATTGCTTGGGGACAGGCCAGGGCAGGGCAGGGCTCTGGCAGGGAG
GCTTATCATATGGAGCGAGGTGTTGGGGAGGGGGCAGGGCAGGGCTGTCAGGGAGGGAGAAGAGAC
TGAGGGGCTGTGACCTCTGAGGCCCTCAGGCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGCTCTC
AGCTGGGGGCTGGAGGTCTGGCTGAGGGGAGGGCTTCACGCCACCCACCCCTGGCCCTGGCAGCTGGTAG
TCCATCAGCACAAATGAAGGAGACTGGAGAAGAGGAAGATAACACTGTTGCTCTGTTCAAGCTGTTGCA
TTTCCCCCTGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGGGATTATAGCAAAGGCTAACGCT
AGTTTACTCTGGGGGTTAGGGAGGCCAAAGGCTAAATAGTTAAGTAGGTGATGGAAGATGAGATTACCTCA
TTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTTGAGAGACACCTGAGAGAAAGGGAGGG
TCAACAAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCACTGC
AGTCCCAGCTGTGTTCTACCTGGTGTAGAAGTGTCTGGTTGCTGGCTGCCATTGCTCTGAGTGG
GCAGCCCTGGGCTTGGGCCCTCCCTCCGGCCCTCAGTGTGCTGTCAGAAGCTCTGGGTTCCCTCAAGTG
CACGAGGGGTTAGGTGCTGTCAGGCTCAGTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC
TCTCAGGGGGCAGCTCTCCATGGCAGGCATCCCTGCTGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG
GGCTGCTCCCCCAGAGGCCAGCTCTGCTGGGGAGGCCATCAGGTGTTGCTGAGTCCATAGCCT
TCTCAATGTGTGTCACCCGAACTGGGAGGGAGGGAAACACTGGGTTAGGACCAACTCAGAGGCTGCTTG
GCCCTCCCCCTGACCGAGGGACATCTGAGTTGGGCTACTCCCTGCTGGCTAACGGTAGGGAGGCCCTCTC
AGATTGTTGGGGCACATTGTGAGGCTGACTTCTGCTGGAGCTCCAGTCAGGAGGAAGAGCAAGGCCACCT
TTGGGATCAGGTGCTGATCAGTGGGCCCCCTACCTCAGGCCCCCTTCCCTGGAGCACCTGCCACCTGCC
CAGAGAACACAGTGGCTCCCTGTCGGGGCGCTTCTGGAGGAGCTGACGCCAGGTGCAACTGTTGAG
GCCTCTGCTGCGGCTGCAATGGATGCAAGGGCTGCAAGGCCAGGTGCAACTGTTGAGTGGAG
CGTCTGAGGCTGGAGGTGACCTGAGGAGGGAGTGGAGGGTAACATTCCATTCCCC
TCATGTTTGTCTTACGTTCTCAGCATGCTCTTAAACCCAGAAGGCCAATTCCCCAAGGCCATT
TTCTGTCTTATCTAAACTCAATATTAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKCPTVFPPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFPERYLNFPDLSLPESSQDSNDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACAGAGAGAGACAGAGGAGGAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAACGGCCCAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAACGTCAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTGGAGAAGGCCAGACCCCTGG
 GCACCTCTCCCAAGCCAAGGACTAAAGTTCTCCATTCCCTTAACGGTCTCAGCCCTCTGAAAACCTTGCC
 TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAAGTGC**ATG**TCCAGACAGGCTCGCATCCCAGGGAGGG
 CTTGGCAGGGCGCTGGCTGTGGGAGCCAACCTGCCTCTGCTCCATTGTGCGCCTCTCTGGCTGGTGTG
 GCTGCTCTGCTACTGCTGGCCTCTCTGCTGCCCTCAGGCCGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGAT
 CGTGTTCAGAGAAAGCTCAACGGCAGCGTCTGGCTGGCGCCCTGCCAGGCTGTGCGAGGCTGACAGTGCAGTA
 GGCTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCGGCTGTGCGAGGCTGACAGTGCAGTA
 CCTGGGCAGGGCCTGAGCTGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTCTGCACTGGATGGGGAGCCCTGTTAGCGTGTACAATATGGGGGGCTGAACCTCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGACCTGGGCTCACATCCTACGCCGAAGAGTCC
 TGCCAGGGTCAAGGTCCCAGTGCACAGCTCCTCTGGAAGCCCCAGCCCCAGACCCGAAGAGCCAA
 GCGTTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGCAGATGACAAGATGGCCGATTCCACGGTGC
 GGGGCTAAAGCGTACCTGCTAACAGTGTGGCAGCAGCAGCCAAGGCCCTCAAGCACCCAAGCATCCGCAATCC
 TGTCAGCTTGGTGGTACTCGGCTAGTGTGATCTGGGTCAAGGCGAGGAGGGCCCAAGTGGGCCAGTGTGCTGC
 CCAGACCCCTGCGCAGCTCTGTCCTGCCAGCGGGCCTCAACACCCCTGAGGACTCGGCCCTGACCACCTTGA
 CACAGCCATTCTGTTACCCGTCAGGACCTGTGTGGAGTCTCCTACTGCCACACGCTGGGTATGGCTGATGTGG
 CACCGCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGGCTCAGTCAGCCTACTGCTGCTCA
 TGAACCTGGGTATGCTCTCAACATGCTCATGACAACACTCCAAGCCATGCATCAGTTGAATGGCCTTGAGCAC
 CTCTGCCATGTGATGGGCTGTGATGGCTCATGTTGAGGACTCTGGTCTGGGCTCCATTGAGGACTGCCGTT
 CATCACTGACTTCTGGCAAACTGGTATGGGACTGTCTCTTAGACAAACAGAGGCTCCATTGCACTGCTGT
 GACTTCTGGCAAGGACTATGATGCTGACCGCACTGGCAGCTGACCTTGGGGCCACTCACGCCATTGTCC
 ACAGCTGCCGCCGCTGTGCTGCCCTCTGGTGTCTGGGACCTCAATGGCATGTGCCAGACCAAACA
 CTCGCCCTGGCCGATGGCACACCCCTGCCGGCCACAGGCCCTGCATGGGTGGTCGCTGCCACATGGACCA
 GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGCTCTGGGACCATGGGTGACTGCTCTGGACCTG
 TGGGGTGGTGTCCAGTCTCTCCCGAGACTGACGAGGCCCTGTGCCCCCGGAATGGTGGCAAGTACTGTGAGGG
 CCGCGTACCGCTCCGCTCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTCCCGAGGAGCA
 GTGTGCTGCCTACAACCACCGCACCGACCTCTCAAGAGCTTCCAGGGCCATGGACTGGGTCCTCGCTACAC
 AGGCGTGGCCCCCAGGACCACTGCAAACACTCACCTGCCAGGCCGGACTGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTCCTGGACAGCTCCTCGGTCTGTGTCAGGCCGATGCATCCATGCTGG
 CTGTGATCGCATATTGGCTCCAAGAAGAAGTTGACAAGTGCATGGTGTGCGGAGGGACGGTTCTGGTGCAG
 CAAGCAGTCAGGCTCTTCAGGAATTCAAGGTACGGATAACAACAATGTGGTCACTATCCCCGCGGGGCCACCC
 CATTCTGTCCGGCAGCAGGAAACCTGGCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCTA
 TGCCCTCAATGGTGAATAACAGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGCAGTCAGCTTGCCTA
 CAGCGGGGCCACTGCAAGCCTCAGAGACACTGTCAGGCCACTGGCCACTGCCCTTGACACTGCAAGTCCT
 AGTGGCTGGCAACCCCCAGGACACACGCCCTCCGATAACAGCTCTCGTCCCCGGCCACCCCTCAACGCCACG
 CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGGGCCCTGGGGCCAG
 GAAA**TAA**CTCACTATGCCGGTGCCTTCTGGGACCGGGCTGGACTTAGCTGGAGAAAGAGAGACTT
 CTGTTGCTGCCATGCTAAGACTCAGTGGGAGGGCTGTGGGCTGAGACCTGCCCTCTGCCCC
 GCGCAGGGCTGGCCCTGCCCTGGTTCCTGCCCTGGAGGAGCTGATGGTTAGTGGATGGAAGGGCTGACAGAC
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCCTGGGCTCACAGGAGGGAGGGGAAGGCAGGGAGGGCCCTGGGG
 CAGTTGATTTATTAGTATTCACTTTATTAGCACCAGGAAGGGACAAGGACTAGGGTCTGGGAA
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGCTAGGAATCCAGGGTGGTGTGATAGGTATAAGGGT
 TGTGATGCGTGTGTGTGAAAATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTC
 TCCCTGAATTTATTGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTT
 TTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 GCACAATCTCGGCTCACTGCATCCTCCGCCCTCCGGGTTCAAGTGATTCTCATGCCCTGCCTGAGTAGCTG
 GGATTACAGGCTCTGCCACCAGCCCAGCTAATTGGTTGTTGGAGACAGAGTCGCTATTGTC
 ACCAGGGCTGGAATGATTCAAGCTACTGCAACCTCGCCACCTGGGTTCCAGCAATTCTCCTGCCCTAGCC
 CGAGTAGCTGAGATTAGGCACCTACCAACGCCGCTAAATTGGTATTGGTAGAGACAGGGTTTCAC
 CATGTTGCCAGGCTGGCTCGAACTCTGACCTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGGATT
 ACAGGCGTGAAGGCCACCGTGCCTGGCCACGCCAACTAATTGGTATTGGTAGAGACAGGGTTACCATGT
 TGGCCAGGCTGCTCTGAACCTCTGACCTCAGGTAATCGACCTGCCCTGCCCTCCAAAGTGTGGGATTACAGG
 TGTGAGGCCACCGCCGGTACATATTAAATTGAATTCACTATTGATGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCTTAACCTCCATGTCTGAGCATTAGATTCTCATTTGCCAATAATAACCTCCCTAGAAG
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAGGAAA

FIGURE 180

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVPGSGAPARLLCRLQAFGETLLEQDSDGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAAKAFKHPSIRNPVSLVVTRLVIILGSGEEGPVQGPSSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVFPGKDYDADRQCQLTFGPDSRHCPCQLPPPACAALWCSGHILNGHAMCQTKHSPWADGTPCG
PAQACMGGRCMHMDQLQDFNIPOQAGGWGPWGPGDCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDVPRYTGVAPQDQCK
LTCQARALGYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTIPAGATHILVRQQGNPGHRSIYLALKLPLDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSHGHLAQPPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAACCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGTTGCTGGCCCTAACTCT
 AATTGTCCTGTTGGGGAGCAAGCACTCTGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAAGCGGAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACTGGCATCTACTCGTGGTCTTCAAAAATGTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTCTTGAAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTTGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGT
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGGAAAGAACTTCCAATAATGACTATACTG
 AAAATGGAATAGAATTGATCCCAGTGGATGAGAGAGGTTATTGTTGTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTACATGCCTGTAAGTGGTGGTGGCCC
 GCATGCTGGGGAGGGT**TAA**TAGGAGGTTGAGCTCAAATGCTAAACTGCTGGCAACATAT
 AATAAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTGTAGGTAATTCCCTCTTCATGTTCTAATAACTTACATTATCACC
 AAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKSKICKSLKICGLVFGILALTLIVLFWGSKHFPEVPKKAY
DMEHTFYSGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEEDLHFPAKEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTCTGGGCTTCCT
 GCTCAGCTTCCCTGGGCATGGTGGGCACGTTGATCACCAACATCCTCACGCCGTGCCTACCTGAAAGGGCTCTGGATGGAG
 CAGCGCACGTGGGCACCAACATCCTCACGCCGTGCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCCCTCATGGTCATCTCCTGCCTGCTCTGGGCATAGCCT
 GCGCCTGCGCCGTATGGGATGAAGTGACCGCAGGACACCCGCCAAGGAC
 ACCTTGCCATCCTCGGCGCACCCCTTTCATCCTGGCCGGCTCCTGTGCATGGTGGCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTATTGGT
 GGCACCCCTGCTTGCCTGTCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTCTCCCTGGGCTGCTGTGGCTGGGTCCCCGGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAATGTCTTAGAGGCACAGGGACAGAGGGGAAATAAGAGGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATATAT
 TTATGTGGGTGATTGATAACAAGTTAATATAAAGTGAATTGGGAGTTGGTCAGTGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCAGGATGTGGCTGTTATGAAAAAAA

FIGURE 184

MASTAVQLLGFLSFLGMVGTLLTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYR PYQAPPRATT TANTAPAYQPPAAYKDNRAPS VTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCAGGGCGGGCGGCCAGGAT**ATG**TCCACCACATGCCAAGTGGTGGCGTTCTCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCCTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTACCGAATGCAGGCCATTTCACCACCTGGACTCCAGC
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGCCTGGTGCCATTGGCCTCC
 TGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTGTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACCTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGC GGCTCTGTTCTG
 GGCTGGGTGCGCTGGAGGCCTCACACTAACATTGGGGTGTGATGATGTGCATGCCCTGCCGGGG
 CCTGGCACCAAGAAACCAACTACAAAGCCGTTCTATCATGCCCTAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTGGTCCAACACACAAAAACAAGAAG
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTATCCTCCAAGCACGACTA
 TGTG**TAAT**GCTCTAACAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTACCCAAA
 AACAAAGGAGATCCCCTAGATTCTTGCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTCATCTTGGAGAGGCCAAATGGTCTAGCCTCAGTCTGTCTCAAATATTCC
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCAATCCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC
 ATTTGATGATTTAGACAGACTCCCCCTTCCTCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTATCCCCAAGAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTATT
 CTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCAGGCCATGATCGGTTTCTTACACTG
 TGATCTAAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTG
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGCTCTAGATGAATGAGAAAATTATTTTTAAT
 TTAAGTCCTAAATATAGTTAAAATAATGTTAGTAAATGATAACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCACAAATAACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCCGGAGGCTGAGGTGGAGGATCACTTGAGGCCAGGG
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFT
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGGMGVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTCTGTGGCACAGAGAACCCCTGCTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**GCAACCCATGCCTAGAAATCGCTG
 GGCTGTTCTGGTGGTGGAAATGGTGGGCACAGTGGCTGTCAGTGTGATGCCTCAGTGG
 AGAGTGTGCGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCCGGACCTACAGGCAGGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC
 TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTTCCCCAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGC
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTTAACTTAACTAAAGC
 CATGCAAATGACAAAATCTATATTACTTTCTCAAATGGACCCAAAGAAACTTGATTAA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTCTAAGGTGGTTCAAGCATCTACTCTTTATCATTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATATCTCACATAGAGACATGCTTATGGTTTATTAAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTCAAGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATTAATGTCCTCCATTATAATGA
 AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTCCAGAGGCTTTTT
 TTCTGTGTATTAAATTAAACATTAAACGAGATATTGTCAAGGGCTTGCATTCA
 AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGTG
 GTTTAGGAAAGTGAAAATATTGTTGTATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATGTATGGATATATTAAATAAGTATTGAGTACAGACTTGGAGGTTCATC
 AATATAAAATAGAGCAGAAAAATATGCTTGGTTTCAATTGCTTACAAAAAAACAACA
 ACAAAAAAAAGTTGCTTGGAAACTTCACCTGCTCCTATGTGGGTACCTGAGTC
 TCATTTGTTCTGTGAAAATAAATTCCCTTGTACCATTCCTGTTAGTTACTAAA
 ATCTGTAAATACTGTATTGTTCTGTTATTCAAATTGATGAAACTGACAATCCA
 AAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTATTGCTTACATT
 TTAATAAATTGTACATTCTAATT

FIGURE 188

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

DRAFT
DO NOT DISTRIBUTE

```

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGCTGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGGAAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTGCTGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCGCCTGGTGCACCTCTGGGA
TTGTCTTGTCACTCAGGGGCCTGACGCTAACCCCCGTGTGCTGGACGGCGATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCAGGGAGCTGGGGCCTCCCT
CTACTTGGGCTGGCGGCCTCAGGCCTTTGTTGCTGGTGGGGTTGCTGTGCTGCACTT
GCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGCCCGCTACTAACATCTGCCCT
GCCATCTCTCGGGGGCCCTGAGTACCCCTACCAAGAATTACGTCTTGACGTGGAGGGAAATG
GGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGGTT
CGTACCTTTGTTCTGCCTCCTGCTATTTCTTTGACTGAGGATATTAAAATTCAATT
GAAAAGTGGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTCACCTTGG
ATGATGGAGCCAAGAGGGGATGCTTGAGATTCTGGATCTGACATGCCCATTTAGAAGC
CAGTCAAGCTATGGAACTAATGCGGAGGCTGCTGCTGTGCTGGCTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCTGCTGCTGGAGCTCCTCTTCAACCCCTGGAAAAACAAATCATCTG
CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCAACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTGACCTCTGTTCCGTCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
TTTGTTAGTGCA

```

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVTLIIPVCWTAHAIIRDYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAIISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTTAGACTCAAAAGGCTCCACGTTCTACATCTTG
 AGCATCTTCTACCACCTCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCC
 TTGCAAATTGCTGGGCTGGTCTTGGGTTCTGGCATGGTGGGACTCTGCCACAACCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGCAACATTATTGTCTTGAGAGGGCTC
 TGGGAAGGGCTCTGG**ATGA**ATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGGCTCTCCGCCTGCCCTGGAAACAGCCCAGGGCCCTCATGTGTGGCTG
 TTGCTCTCCTTGATGCCCTGCTTATTGGCATCTGGCATGAAGCAGGTCCAGTCACA
 GGCTCTAACGAGAGGGCAAAGCATAACCTCTGGAACTTCAGGAGTCCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTAGAACGAGAGCTGGAGCAGCACCTTCCTGGCTGGCA
 AGCGCTGCTGCTCTTCATTGGAGGGGTCTGCTTGTTGGATTTGCTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGCT**TAA**TGCCTCCTTGCTCCAAGT
 ATGGACTATGGTCAATGTTTATAAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAACTTGCTTATGCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAACATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPTHDKRRNTTMSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGAATGAATGTCATTGTGTACC
GAGAGCTTGAAGAGTAATGGAAGAGTCAGTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTGAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGC~~GG~~CCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGGGCCTGCTGTCC~~TG~~GGCCCTGACC~~GGG~~C~~TG~~GGC~~G~~CTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTCAA
AAACGAGAAGCACCTGTTCCA~~A~~CTAAGACTAAAGTGGCGTTGATGAGAATAAAGCCAAAGA
ATTCC~~T~~GGCAGCCTGAAGGCCAGAACGGCAGCTGTGGGAC~~GG~~ACTCGGCCGAGGTGC
AGCAGTGGTACCAGCAGTTCTACATGGGCTTGATGAAGCGAAATTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCTTAATGCCTTACACTACTTGGTTCTGATTGCTCTATTCAGCAGAT
CTTTCTACCTACTTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTT
TGATATTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTGTTAAAAGA

FIGURE 196

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLCWGPPIISGNKLKMLQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

www.ncbi.nlm.nih.gov

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTGCCTGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC
GGTAGCGCGGGCAAGGCAGGCGCC**ATG**ACCTGATTGAAGGGTGGGTATGAGGTGAC
CGTCCTTTCTCGGTGCTGCCTGCCTCTGGTCTGCCCTGCCTGGTCTAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCGTCAGGGACCCAACGCCATCCCAGCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGTTCACAGCAACACCAGCAG
CCCCGGACTCCCCGAGGAGCCCTCGTGTACGGCTGAAATTCTCAATGATTAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCCAGGAGATCGGTCCC
CCAAATCCCCCTGCCGCCGGGTCCGAGCCGCCCTCCGGCTGGAAATCGGCAGCCT
GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTCCCTGACGCCACTCTGGCCTGGCCGGCTTCACCCCTGCTCCTCAGTCTCCTG
GCCTTGCCATGTACGCCCG**TAGT**GCCTCCGCCGGCGCTTGGCAGCGTCGCCGCCCTCC
GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCAGGCCCTCTCCGGCCTG
CCTCTCCGCTGCCCTGGAGCCAGCCCTGCCCGCAGAGGACTCCGGACTGGCGGAGG
CCCCGCCCTGCCACGCCGGGCTCGGGGCCACCTCCGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTGGGGTCCGGCATCTGCTGTCGCTGCCCTGGCCGGAGAGCCG
GGCCGCCCGGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
AGCTCCTTGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTGAAGGGAGCGGGAG
GGGCAGAGGAGTTCCCCGAAACCGTGCAGATTAAAGTAACGTGAAGTTAAAAAA

FIGURE 198

MTLIEVGDEVTLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPGSGLEIGSLLLPLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAACGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGGTCAGCAGC
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCACTCAGGGATTCTTCATTCTTCTTCCACTGCCTCCA
CTTCATGTTATTTCTTCCCTCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTCTGGCTTCCCTTACTCCCCTGGACCCAGTCCCTGGTTCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSLENLCHVDCQDLLNPNLLAGIHCARKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGAACCTATTATACAAAGGGGAAAGAACACCTGAG
 CAGAATGGAATCATTATTTTCCAAAGGAGAAAACGGGGTAAAGGGAGGGAAGCAATT
 AATTGAAAGTCCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACACTGGGTCTGTGGTTCTGATTGTAAGTGAAGCAGGTCTGCACACGC
 TGTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACCTCCAGGTGGAACAAGCA
 ACCATGTTCTGCAAGCTGAAGGAGCCTGGAGCAGGAGAAAGCTAACCTGAACATGAC
 CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CCTAAGGAAGCGATAACAGGCACAGACCATG
 CAGACTCCAGTCCCTCTGCTGCTCTGATGCTGGATGCGTCCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCCCTGCACCAGACTGTCACAGCCCAAGGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTATCTACTGCGGGAGGATCAGC
 TGCTGGTGGCGTGGCTTACCCCAGGCCAGAAGGAACCAAGAGCCAGGGCAGGAGAGGTGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTTCTGAAGAAGAGGAGTTGACCCGTTCAGCCTGGACCCAC
 GTGCCCTCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGG
 CACCCACTGTGTCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCTGGTCACTCTCCTGCGACTGTACACAGCATTGACACAGTGC
 CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACACTCAAG
 TCTGCTCTCAGGAATATGTGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCAGTGGTATCTCGGTGATAAGATGTGATTGACTGGAAGACTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGGACTGGAAGCTGGATTCCACTGGGAAC
 CTTGCCAGAGCATGTGAGGAAGGCCCTCAGTCCCCCATAAGCCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCATGGACAGACATTACTTCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCAGGTGGTAAAAACCTCGAACTGTCTTCAAGGCCCTGGCTCTGGTG
 GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACCAAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGG
 GTCATCAAAGAACCTTCTACAAGCATGCCAGAGGCCCTCTCCTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTGCAGCTGCAAAGGAGACTGGGTGTCGGACATTCCACTGG
 TTTCTGGCTAATGTCACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA
 GCTCCACAAACACTGGACTGGGCTCTGTCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCTTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTCACTTGGCAGCCCACAGCACCTGTGCTTGCTGAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCATCCACCAGCAGCACTGGACTTCCAGG
 AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTGAAGAAAAC
 AATAAAGATTGTACCTGCGCCGTGTGATGGAAAAGCCGCCAGCAGTGGCATTGACCA
 GATAAAATGCTGTGGATGAAACGA**TGA**ATGTCATGTCAGAAGGAAAAGAGAATTTGCCATC
 AAAATCCAGCTCAAAGTGAACGTAAGAGCTTATATATTGATGAAAGCTGATCCTTGTGT
 GTGTGCTCCTGTGTTAGGAGAGAAAAAGCTCATGAAAGAATATAGGAAGTTCTCCTT
 TCACACCTTATTCATTGACTGCTGGCTGCTTA

FIGURE 202

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMVVAMLPFHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYEYSPLEGPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFFQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFWFLANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDFQENGMIHVILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTCCCACCTCCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTTCTCATCCTCCCTCGAACCCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGGAGGGCCCTCGGCCAACGTATGTGCGTGAGGAGCAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTGAGGAGGGGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCCAACTCTGCCAATCCGG
 ATTCTGGACTATGGTTTGCAGCCCTCATGGGCTCGCAACCCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTGGAGAGGCCACCTGCCACCCCTGCCATTG
 CTGTTGGGGGCCGTGGGAAGGTGTGGACCCAGCTCTATGTACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCAGTGTGTGGGGCTTCGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCCTGGGATGCCCAAGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGCAAC
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCACAGCCCTGCCCTCCAAGGGGCTGGACAGCTCCTCTGGGAGGCACCCCTTC
 CTTCTCCCAGTCTCTCAGGATCTGTGTCCATTCTCTGCTGCCATAACTCCAACCTGCC
 TCTTGGTTTCTCATGCCACCTTGTCTAACACTCTGCCCTTTAACCTGATTCCC
 CCTCTTGTCTGAACCTCCCTCTATTCTGCCCTACCCCTGGTCTGACTGTGCCCTT
 TCCCTCTCCTCTCAGGATTCCCTGGTGAATCTGTGATGCCCAATGTTGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCAGTGGGTGGGCAGCTGTGGGA
 GCTGGGCCACAGGGCTCTGGCTCCTGCCCTTGACACACCACCGGAACACTCCCCAGCC
 CCACGGCAATCTATCTGCTGCCCTCTGCAGGTGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGCCCCACCCCTGTGCACTCACATGAAAGCCTGACACTCACCTCCACCTTCAC
 AGGCCATTGACACGCTCTGCACCCCTCTCCGTCATACCGCTCGCTCAGCTGACTCT
 CATGTTCTCGTCTCACATTGCACTCTCCTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCCGGCTGATGTTGGTGG
 TGTGCGCGTGTCACTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC
 GTGCTGCTCAGAGGTGGGTGGAGGTGAGCTGGGGCTCCTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCCACACCATTGTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCAGACTTCACCCCCAGCCCA
 CTGCTAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGACTCCATTGCCCTCCCTTCCTACAGTCCCTTTGTCTGTCTGCTGGCT
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCTTGGGCCCTCCCTAACCTCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTGCCTCCAAGTCTACCCCTCCCTCCGGACTCCCTCTGTCCCTCCCTT
 CCTCCCTCCTCCACTCTCCTCTTGTCTCCCTGCCCTTCCCTGGCTCCTAGGCT
 CTCCCTCCTCTCATGGTTTTCCACCTCCTCCCTCCCTGGCTCCTAGGCT
 GTGATATATATTTGTATTATCTCTTCTGTGGGTGATCATCTGAATTACTGTG
 GGATGTAAGTTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPASPQRLLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCGCGCAGTCCTCCGTGCGTCCGCCGGCGCTGCCCTCACTCCGGCCAGGATGG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCCTGCCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGCCGGCGCTATCGCGGCCATCGTATGCCGCCCTGCTGGCACCTG
CGTGGTGCTGGCGCTCGTGGTCGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCCGGCCGGCCGCGACTCGGCAAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

TGTGATTAAAGTCCCTGATGTTCTC

GGCGTGGTGGTGC CGCGCTGAAGGGTGTGGCGAGCAGCGTCGGTGGCGGGCG
 CGGGCCGGACGGG**ATG**GCCTGCTGCTGCCTGGTGTGCCTACGGCGCTGGCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTCTACCGCCACCATGTGA
 ACTTCAAGTCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGCCATCCCCGCAAGATCACCCGGAGAACGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCCAGGGAAAGATGTACTTCC
 CCGGGTATTCCTCAACGAGCTGCAAACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAAGGCAGCTGGGAGGGAGGGAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTCCCTCCGGGCATGGACACACATACTGAAAACCAGGGCGCAT
 CGACTGTCAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCCTGCAACAACACTGCACAG
 ACTCGCACGTCGCTGCTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT
 GCCAGGGCCCTACTGTCCTGGGTCCCAGGCTCTCCTGGAGGGGCTCCCCGCTTCCAC
 CTGGCTGTATCGGTAGGGCGGGCCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT
 CCCACAGGTCTCGGCCAGTGGAAAGTCAGCTGTCCAGGGCTCCTGAACTAATAAAC
 TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTTGCGCAGGAGGCAGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCTCAGCTGGAGGCAGGATCTTCTAAAGGTCCCCATAGGGTCTGGTTCC
 ACCCATCCCAGGTCTGGTCAGAGCCTGGAGGGTCCCTACGATGGTTAGGGTGGCCCC
 ATGGAGGGGCTGACTGCCACATTGCCCTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
 CCTGACCTGGACTTCAGGGGAGGGGTAAAGGGAGAGAGGGAGGGGGCTAGGGGCTCT
 AGATCAGTGGGGCAGTGCAGGTGGGCTCCCTATACCTGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACCGCTCCTCTGCCTCTCCTGG
 CCTGGACACACAGGCCACCCGGCCTGTGAGTGACCCAGAGAAGGGAGGCCTGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCAGCGGGCTGCACACCTCGGACATCCCAGGC
 ACGAGGGTGTGAGTGTGGCACACATAGGACCAACAGTCCCAGCTGGAGGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGACATGGAGAGAGCTGAGGCAGCCTCGTCTCC
 CGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTGGCCAACCTGACCT
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGGCAAC
 GTGGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGCTGCTGCTGC
 CTCAGGACCCCTCTCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGCGGGAGG
 GAGGGAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCCGCAGAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIAPAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAAIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

TOP SECRET//SI

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCCAGGATTAGAAATACCAGCAGTGCCCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAAACATCACTGGAACACCATCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAAGATTCACTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATAACCAGAAGGCAGCCAAGCTCTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTTACCAAGACTCTAGATGACGAGTGGATACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTCTCCTGGAACATACATATGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACACTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCAACACACACACAGCTTCATTCCGTCTAAAATCTGTTCTC
 TTCTCCTTCTTAAATTCAATCCTCACTCCCTATCCAATTCCCTTATCGTGCATT
 CATACTCTGTAAGCCCACCTGTAACACACACCTAGATCAAGGCTTAAGAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTGTCATTAAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTCATAAGCACATGTCCGTCTGACTCAGGATAAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTAGCATCTCCAACCTCC
 TATGTAATCAACAACCTGCATAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAAEVAEEVKESSDGPAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLVNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDGMKENGKVISFFKLKESQLPALAIYQTLDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGGGGTG
 GCGGAGAGATCAGAACGCCTCTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACCGCGCGCGCGCGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGG
 GCAGGTGATTGCAGCCCCAGACAGCCGGCGTGGCTGTGGTCGGTGCTGGCGGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGAAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGCCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAGAGAATTGCGCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTG
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGCCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTGTAAAGAGTCTGCCTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCCTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTATGCGGATATCCGAAAGAAT**TAA**GAGAACATACCTAGAACATATC
 CTCAGCAAGAAACAAACAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGAAGGACAAGTACACGTGACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTTTTGACTTTCTTT
 AGGTCAATTACAATTGGGAGATTTCAGAAACATTCCCTTCACCATCATTAGAAATGGTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTACAGTACGTTAGCAGTACGTTAGTGTCTGCCGCTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTTGAAAGTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTAGACTTAAAGTTGCACCCCTG
 AAATGTGTCAATCAATTCTGGATTCAATAGCAAGATTAGCAAAGGATAATGCCGAAG
 GTCACTTCATTCTGGACACAGTTGGATCAAACTGATTAAGTAGAAAATCCAAGCTTGCTT
 GAGAACTTTGTAACGTGGAGAGTAAAAGTATCGGTTTA

FIGURE 212

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLCKFKS
TSTTGGLTSVWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWWVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSINKSESVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGCTGCCGCC
 CCCGGGGCTTGGCCTCAAGCTGCGGACGACGCCGGTCCATCAGCGGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGTCGGGGCTCGGGCTGGGCTGGGCTGGCGCTGGGTGAAGC
 TGGCAGGTGGCTGAGGGCGCGCCCCGGCGAGTCCCCCGCGCCCCGACCTGAGGCG
 TCGCCTCTGGCGAGCCGCCACAGGAGCAGTCCCTGCCAGAGCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 GCCGCCCTGCTCCAGGTGCTCGCCAGAGCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAGAGACAGT
 TATGCGATTGCTAGCATCAGCAAAAGTCTCACCATGGTGCTCTGCCAATTGTGGAG
 CAGGGAAACTGGATTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCCATTAAAGTGGATTG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTGAAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTGTATTCA
 ACTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTGGA
 CTATATGCAGAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACCTCTGCTGTCTAGCTATATCGCATC
 TTAACACTATTTATTAATTAAAAGTCAAATTCTTGTCTCATCTGTAAAGTGAAGGAAGTAAAACA
 CACATTGGAGCTTCTACATGTCTGTTCTCATCTGTAAAGTGAAGGAAGTAAAACA
 TGTTATAAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQAGLPPPLGHGWGGLGLGLALGVKLAGGLRG
AAPAQSPAAPPDPEASPLAEPPEQQSLAPWSPQTAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQNEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
 AGGCTGGTGGAAAGAACCGAGATGGCGGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGCTGCCGGCCGGACT
 GGTGCGCGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACCTCCGGAAAGCGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGAGCTCAGCGAGGAGGAGCGGGC
 CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCCTCCTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGACCTGTCGGACCAGCTGACCTGACGTGGATGTGCCGGCAACGTGGTGGC
 GTGTCGGTGGTACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTCGCCAATACTGGATGTACATCATTCCGTCCTGTTCCCTCATGATGTCAGG
 AGCGCCAGACACCAGGGGCCAGGGTGGGGTGGGGTGGGGTAGTGGCC
 TTTGCTGTGCCACCCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTGAAATGTG
 TGAACGTTTGAAAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
 TCCTGATGTACAAGCTTGTGATTGAAATTCACTGCTCACTGATACTGTTATTCAAACCCAAG
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT
 TAAACTGTCCCCAGATCGACACGAAAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAVTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSQLWNQQDGTLSLSQRQLSEEERGRRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGGCGTCCCCGAGACCGGGGAGCAGGTGTCGTCGGGGGCCACC
ATGCTGGTACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAACCT
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTATGTCTG
 TGGCCTGCCTCTACAGCCTCTTGGCCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC
 GCAAGAATTCTTGTGTCCTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCGAGCAGCTGGTGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC
 CATCCCTCTCCCTGGCTCTGGCAGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCTGCGAACCGCCGC
 GTGCTGCTGGCACCATAAGCTCTATTGAGAGTGTCACTTCATCTTGTCTTGTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTCTCCAGCTTCATGG
 CAGCCAGCCTGCTGGCTCTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCTGCTGTGCTCATCGTCGCTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCCAGCATGAGCTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATGAAAAACAGGCACTCGAATATGTTCAGCATTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTGAATTCCAGCTATCGGGATTGTACAGATCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAGTTCCCTGTGTTACTCCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAFAWNHVLA
VAEEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATS
KRYHLQPMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVI
PETEQAGVLNWFRVPLHSLACLGLLVLHDSRKTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGCGGGCGAGAGGAAACGCGCGCCGGGCCGGCCCTGGAGATG
GTCCCCGGCGCCGGCTGGTGTCTCGTGTCTGGCTCCCCCGTGCCTCGCGGCCA
CGGCTTCCGTATCCATGATTATTGTACTTTCAAGTGCTGAGTCCTGGGACATTGATA
TCTTCACAGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTGGAACAGCATGGCTGCCATGGCCATCATT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAAGAGTTGCTTGGACATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAACCCACTGGCCTCCCTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCAGGGCTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCTGAGAGCCATCTGTGACCTGTACACT
CACCTGGCTCCAGCCTCCCCACCCAGGGTCTGCACAGTGACCTTCACAGCAGTTGG
AGTGGTTAAAGAGCTGGTGTGGGACTCAATAACCCCTCACTGACTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWL PACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

www.glycosylation.com

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCATCCTCCTACTGGCCTACGGCTGTCAGTCGGACTAGGTGGCAG
AGGCCAACCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGTGCAGCATCTACAAGGACAACAACAAAAGCAGCATACTGTATGGAT
TTATCTAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTNAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGC
HCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVF
NVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTGCCGGCACACCAGACGCCAGTCACAGGCAGAGCCCTGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTCACGCTTGCCTCCTGGGGGCCACCTGGCAGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCTCCTGGTAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTGCCTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTGGAGCTTGATGCCAGATCTCCTGCCTACCCCAGCCAAG
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAAGTTAACATCACATACTC
AGCAAACTCACCGTGGTCG**TAG**GGTGGGTATGGGCCATCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAC TGAGTCGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPAGGKYFSTTEDYDHEITGLRVSVGLLVKSQVK
LGDSWDVKGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

www.ncbi.nlm.nih.gov

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAACGTGCTGGCTATGGAATAACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATAACATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTAACGCCCTCCCCACCCCCCAAAAAAAACTGTAAAGATGCAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTGTGATGTTGCTGCGAATGCGGTGTTGGATT
 TATTGTTCTGGAGTGTCTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGCTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGAGCTG
 ACAGGGGCTGTCATGCAACTGCCCTAACGCCAAAGCAGCTAACAGGACGACCTTGAA
 CAATACAAAGGATGGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTTACTGACAATGCTTCTGCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTGCTCCTCGCTATAACAGCCTCAAAACTTAAGTATAAT
 CAATTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTAATGGAATAACGAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTCTTAACAATAACCTTCAGACCTGTGACAAATTACGGAACTTGGATCTGTCC
 TATAATCAGCTGCATTCTGGATCTGAACAGTTGGGGCTTGCGGAAGCTGCTGAGTT
 ACATTACGGCTTAACCTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACATCAATTTCAGCTCAACCTGGCCCT
 TTTCCAAGGGTGGTCAGCCTTCAGAACCTTACTTGCACTGGAAATAAAATCAGTGTCAAG
 GACAGACCATGTCCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAATCTGCAGCGCCTAACCTGGA
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGGTGGAAATATGGGAATGCAGCAGAAATATTGCTCCCTGTAAGCTGGCTG
 AAAAGTTAAAGGTCTAAGGGAGAATAACATTATCTGTGCCAGTCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCAAAGCCGACGTTAACGCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTGCCCCGACGGTGGAGCCACAGAGCCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTCCATAAAATCATCGCGGGCAGCGTGGCGTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAAGCGGTACCTCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAACGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTAAAGCTGGAAATAAGTGGTGTCTTATTGAACTC
 TGGTGAATATCAAGGGAACCGCGATGCCCTCCCTCCCTCCCTCACTTGGTGG
 CAAGATCCTCTTGCTCCGTTAGTCATTCAATAACTGGTCAATTCTCATACATA
 ATCAACCCATTGAAATTAAATACCAACATCAATGTGAAGCTTGAACCTCGGTTAATATAA
 TACCTATTGTATAAGACCCTTACTGATTCCATTAAATGTCGCATTGTTAAGATAAAACT
 TCTTCATAGGTAAAAAAAAAA

FIGURE 226

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHEHNQFSKLNLAFFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRIDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIIICASPKELOGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRRKKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAAGATCCAGACTTTCACTGGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCTGCTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGGTTTGG
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTTGGAGACTTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAACGTGTTGGAAATTCACCTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
 AACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTCA
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAATTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTGATGTGTCAGTGCTATCATACTTTATGCTACAC
 AACCAAATTAAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGTCCATAAAATTATAATTAAACAATAGCCAAAGCCGAGAATCCAACAT
 GTCCAGAACAGAACAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAGGAAAAGATTACAAGTCT
 CAGCAAAACAAGAGGTTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTCCTGGAGCCTCAGGGCTTG
 GCATTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
 AACATCAATAGATATCTAAAAA

FIGURE 228

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLVLA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGC
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGACGCAGCTGACGCCCGCTTATT
 GCTCTCGCTCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCACCGTGACGAGAAC
 ACGCCAGCTCAGTTCTCTTCACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAA
 CCCTCTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAAAC
 ATGAAGAATATAACATATTGAGGATATTTTTTTCAAGTCTGATTGTGG
 TTACCTCAAGTTACCATTTTCAGTCAAGTCTGTTGTTGCTTCTCAGAA**ATG**TTTTTA
 CAATCTCAAGAAAAAATATGTCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT
 TGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAA
 ATTGCTGCTTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTTGTGAATGGCTCAGCAGCCAACACACCACCAATGGTACTAGTGGAAATTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTG
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTACAATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTTAAAGAGAATTGGTAACTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAATCTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATT
 ATTTCTATAACACATTATTTAAGTATAACACGTTTTGGACAAAGTGAAGAATGTTAA
 TCATTCTGTCTTGTCAATAGATGTAACTGTTAGACTACGGCTATTGAAAAATGTG
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAA
 TAATGTTTGAAATCATGACCCAAGAACATGTATTGATTGCACTATCCTTCAGAATAACTGA
 AGGTTAATTATTGTATTTAAAAATTACACTTATAAGAGTATAATTGAAATGGGTAG
 CAGCCACTGCCATTACCTATCGTAAACATTGGGCAATTAAACAGCATTAAAGTT
 GTAAACTCTAATCTTACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTTCACATACATGAATGTTATTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTTCATATTGCTTATTGAGGACTTCCAGGTGTATATAAAA
 TAGGAGGAAGGGACTTGGAGAATGGAACTCTTGAGGACTTAGCCAGGTGTATATAAAA
 GGTACTTTGTGCTGCATTAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTATGAAATTGAAATTGTATAACAGATGCATTAGATATTCAATTATATAATGGCAC
 TTAAAATAAGAACATTAAATATAAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGAAACCCCTAATCTGGTAATTCTAGTATAAAACAAATTACTTTAT
 TTAATTTCCCTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTCAAGTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTAGACTATATAGAATTAGATAT
 TGTATTGTTGTCATTATAATGCTACCACATGTAGCAATAATTACAATTGTTATTAAA
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAAATCTCTCTTCTGT
 CTGTCACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGGCCGGGCCGCCGGGTGAGCGTGCCGAGGC GGCTGTGGCGCAGGCTTCCAGCCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAAACCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTCAGGCTTTGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCTGGGCCACATCATGCCGGTGCCTACCCCTCTGGACACAGCCCA
 CTTGGACCTGTCCTCCAACCAGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCGGGCT
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
 TTCTCCCAGCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTACCCAGCTCACAGCTGGAGCTGAACCTAGCCACAACCAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTACGACGACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
 CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
 TGCCTACCTGAGCCTGGATGGAACCCCTAGCTGTCTGGTCCGGTGCCTCGGG
 CTGGGAGGCCCTACACACCTGCTCTGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTCCGTGAGCTACCGGGCCTGCAGGTCTGGACCTGTCGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGGCACC
 AACCTGGTGCCCTGCCTGAGGCCTGCTCCTCCACCTCCGGCACTGCAGAGCGTCAGCGT
 GGGCAGGATGTGCGGTGCCGGCTGGTGCAGGGCACCTACCCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGCCCCACC
 ATCTTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCTGGCTGCCTCAG
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAAGTGGGAGGCCAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGCCTAGGAGAGGCTTGGACCTGGAGGCCACACCTAGGAGC
 AAAGTCTCACCCCTTGTCTACGTTGCTTCCCTTCCCACTTATCCCCAAGTGCCTCCCTCAT
 ACCAGACTCGGGTCCCCTCTGCTTCCCTTCCCACTTATCCCCAAGTGCCTCCCTCAT
 GCCTGGGCCGGCCTGACCGCAATGGCAGAGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGCCTGAGTGTCCCTTGGGCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCACCCCTCTCATGTGAC
 AGATGGGAAACTGAGGCCCTTGAGAAGGAAAAGGCTAATCTAAGTCCCTGCCAGTGGC
 ATGACTGGAGCACAGCCTCTGCCCTCCAGCCGGACCCAATGCACTTCTGTCTCCTCTA
 ATAAGCCCCACCCCTCCCCGCCCTGGCTCCCTTGCTGCCCTGCTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTACAAGTGGACTCTGGCCTCTGACCAGCT
 GTGCCGCATGGCTAACGTCACTCTGCCCTCGGAGCCTCTGGAGCTTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTCTCACCCCTGGGTGGGCCCCAGCATCCAGACTGGAAACCTACC
 CATTTCCTCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGATCTCCAAGGGCCTCTGGATTGAGTCCCAGTGGCCTGAGCACGACAGC
 CCTTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCCTGGCTGTTCTTAGTCTCATTTA
 TAAAAGTTGTCCTTTAACGGAGTGTCACTTCAACCGGCCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTGTAAGCAGAAAAGGTTGCATTGTTCACTTTGTAAT
 ATTGTCCTGGGCTGTGTTGGGTGTTGGGGAAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCCACAGGGCAGTGAGCTGTCTCCCCCACCTGCCCTAGC
 CCATCATCTAACCGGTCTTGATTAAATAACACTATAAAAGGTTAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQTTRPCFPQGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPPTI
QSLNLAWNRLHAVPNLRDPLRLYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRPELAPS
GFRELPGLQVLSDLGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
QGDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
 AAACAAGTTTGACATTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCGCTGCT
 GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCAAC
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAAGGCTAAGATGAAAGCC
 TCTAGTCTGCCTTCAGCCTCTCTGCTGCGTTTATCTCCTATGGACTCCTCCACTGG
 ACTGAAGACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATG
 GATTTCAGAGATACGGGGCAGTGTGCAAGCCAAGATGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCCATT
 GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTCAATAACCTGCAAGAGGAGGCATGACCCAAACCACCATCTTTACT
 GTACTAGTCTGTGCTGGTCACAGTGTATCTTATTCATTGCTTGCATGAT
 TGTCTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTGTAATATCTT
 TCTGCTATTGGATATTTATTAGTTAATATATTATTTATTTGCTATTAAATGTATTT
 ATTTTTACTGGACATGAAACTTAAAAAAATTACAGATTATTTATAACCTGACTAG
 AGCAGGTGATGTATTTATACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCT
 AGGGGGTTATTCATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTCTTGCATA
 CCAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGGAGGGCTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGGGCTACCGTGGC
 CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAACGAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGATGGTGCACACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCGAGAGGTTG
 TGTGGCAAAAGTGAAGATGAGCATTATCCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGCCAGTTTAGCCAATCCAAC TGACCTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCTGTGGTACATCATGCATTG
 CAAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATAACAA
 AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACTGAAACACTACTTGGT
 ATTGAATACACCACTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGAACACCAGCCATGTCATCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAAGGAAGGGACTTTGTATAAATCATGACTGACTGCTTGATTCAAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLCVVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSRI MNQPRDKQGRGLLYKSSTDCLIQAVQGE GFMSLYKGFLPSWL RMT PWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCAGCGC
 GCCTGAAGTCGGCGGGCGTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTATGC
 TTAAGAAGTAAAAT**G**GCAGGCTCCTAGATAATTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCATGCCT
 TCACACATGTGGTGTATTTCACATTGGCTTCTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCT
 TTCATTGGTTCATGTTGATGTTGGGTCACTTATTGCTTCCATGTGGATTCTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTTCAAATGCACTTA
 TATTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACC**TGA**ATCAC
 TTCTTAAGTCACATTTCTTGTATATTCTGTTAGATAGGTTTATCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTTACATTTATGTT
 TGAGTTTGAAATAGTTTATGAAATTCTTATTTCATGCAAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTATTCTGAGATTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTAGAAGTAACCACTCTGT
 CTCTCTGGCTGGCACGGTGGCTCATGCCGTAAATCCCAGCACTTGGGAGGCCGAGGCC
 CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCAAACCCCCATCTACT
 AAAAATACAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCCAC
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTAAAAAAAAAGACCACTCTCAGTATC
 TCTGATTCTGAAGATGTACAAAAAAATAGCTTCAATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTTGTAACTTATTTGGCCTAAAATGAGGTTTTGGTAAAGA
 AAAAATATTGTTCTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
 AAAGGACTAGTTGAAAGCTCTTTAAAAAGAATTCTCTAATATGACTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDA
AVVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCACTGGGTCAAGGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG
 GGAAGTGGGAGCCTCGAGCCCTGGGTGGAAGCTGACCCCAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTCGCCTCTGCCATCTTGCCATAGTCACGACATGGA
 TGTTTATTGAAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTTTGCGTTAAAATCTGCAGTGGGCCAACGTCGTGGCCCTACTATGT
 GCTTGAAAGACCGCATGATCATGAGTCCTGTAAAAACAATGTGGCAGAGGCCTAACATC
 GCCCTGGTGAATGAAACCACGGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACGGGCTTGGAGCTTAAAGAACAGCCCAGACACAAACAAATACG
 CCTCAGGGTAAAAGCCCCTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAACGCCATTTAGGGTGGC
 TGTGGCTCTCCTCAGCCAGGGCCTGAAGAAGCTCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCCTGGAAAGGTGCTGCAGGTCTGCACGC
 TGTGTCGCGCCTCTCCTCGGAAACAGAACCCCTCCCACAGCACATCCTACCCGGAAAGACC
 AGCCTCAGAGGGCCTCTGGAACCAAGCTGTCTGGAGAGAATGGGGTGTTCAGGG
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTAA
 TTTTGCTGGTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGAT
 CCAGAAACCATGATACCCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACA
 GCAAGAGAACGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTGCCTGTCTAGTCCTCTAGTCCTCAAATTCCAGTCCC
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGCCA
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT
 GACATTGACCCCTGATTGCCTGCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTGGACCTGCACAACAATGCCACACAGTCAACTCTCTGCCCTCACCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTCAAGAAAGGATC
 CCCAGGGGGTCAGAACACCAAGATCAACAGTGAAGCCACATTGAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCCTGGCATTCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAAGATCAGAACAGCTCAGTGCCTCCCTCAACCTAACAGAG
 AGCTGCTCCCAAACAGCTGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTTACCAAGAGTGTGCTGGACAGTTTTATAGAAGGTCCCAGATTCAATGGAACAGCT
 GGAAAAGCTTCAGGGACATTGTTCTCCACAGAACAGAGGCCCTCAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTGCTTCTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTTGGCTGCTCTG
 CCTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAACCGAA
 AGAGTGTGGTCTCACCTCAGCACAAGCCACGACTGAGGCTAAATTCTCTCAGATAACCA
 TGGATGTGGATGACTTCCCTCATGCCCTACAGGAAGCCTCTAAAATGGGTGAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGCTCCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACACTGCAGAGCCTCAGCCTCTCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
 GAAGTTGGATATAACCCAAAGTCCTCTACCCCTCACTTTATGCCCTTCCCTAGATA
 TACTGCAGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATTTTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTCACCAGAGTAAACTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTC
GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTTGTCTCTAGG
ATCAACTCGGTCAATTACACAGCTCAAACCTGCTTGGACTCCCTCCCACAAAATGGCTC
CGGATCAGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTCCTTTAAGTCTG
ATACCATTAAACACAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
AATGACACCTGGTACCCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAAC
TGCACCCACATGTGTACCAATTTCACACAAACTGGAGCCCAGGGCACTATCCTAACGC
TCAGAGGAATTGCCACAAATCTCACGAGCCTCATCATCCATTCTGTTCCGGAGGCAT
CCTGCCACCAGTCAGGCAGGGCTAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAG
GAGCAGGTGTAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCAACTCCCAGTGGC
ACAGATGACGACTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
GGAAGCCACCAAGAATCAGCAAATGGAATT**CAGTAA**GCTGTTCAAATTTCAACTAAG
CTGCCCTGAATTGGTGATACTGTGAATCTTATCATTGATTATATTGGAATAGATTGA
GACACATTGGATAGTCTTAGAAGAAATTAAATTCTTAATTACCTGAAAATTCTTGAAATT
TCAGAAAATATGTTCTATGTAGAGAATCCAACTTTAAAAACAATAATTCAATGGATAAAT
CTGTCTTGAATATAACATTATGCTGCCCTGGATGATGCATATTAAACATATTGGAAA
ACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLP IFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

4 5 6 7 8 9 10 11 12 13 14 15 16

FIGURE 245

GGAGAGAGGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGGCG
 GAGCCAGACGCTGACCACGTT CCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCGCGGCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCGTCAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCAGACGGAGCCCTGGGCCAATGTTATTCCGGTACACCTG
 GGATCCCAGGGATGGATTCAAAGGAGAAAGGGGAATGTCAGGGAAAGCTTGAG
 GAGTCCTGGACACCCA ACTACAAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCT
 TGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGTCTAAGAGTTTGT
 TCAGTGGCTCACTCGGCTAAAATGCAGAAATGCATGTCAGCGTTGGTATTCACATTC
 AATGGAGCTGAATGTTAGGACCTCTTCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAAATATTCACTGCACCTCTGTGGAAGGACTTGTGAAG
 GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGTTGGCACTGTTCAAGATTACCCAAA
 GGAGATGCTTCACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTAATTTCATTGCTACCTCTTTTATTATGCCTTGAATGGTCACTTAAAT
 GACATTTAAATAAGTTATGTATACTGAATGAAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATTCACTTGTCAATCAAAGT
 GGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCAACCTA
 TAATTGGAATTGTTGTGGCTTTGTTCTTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTATATCTGTTAAAT
 AAAAATTATTCCAACA

FIGURE 246

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217